

```

RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
ID Q8UVX5
AC Q8UVX5
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F9D3D351CFEEF3 CRC64;

Query Match 45.6%; Score 273.5; DB 13; Length 127;
Best Local Similarity 48.6%; Pred. No. 1.2e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATVKAICTGVI-NLN 58
Db 24 QDWLTFQKHITTRDWDVDCNLMPTSLF---DCKDKNTFIYSPGVKALCRGVIFSAD 79
QY 59 VLSSTRFQNTCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 80 VLITSEFYSDC---NVTSRCKYKLNKSTKFCVTCENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
ID Q9DFY6
AC Q9DFY6
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 4.1e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATVKAICTGVI-NLN 58
Db 24 QNWETFOKKHLTDRDVKDAEMKALF----DCKQNTFIYARPGRVQALCKNIIVSKN 79
QY 59 VLSSTRFQNTCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSTDEFYSDCNRIKL---PCHYKLNKSSNTICITCENKLPVHFVAVEECP 128

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 40.5%; Score 243; DB 13; Length 129;
Best Local Similarity 42.5%; Pred. No. 4e-20;
Matches 48; Conservative 25; Mismatches 30; Indels 10; Gaps 5;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATVKAICTGVI-NLN 58
Db 24 QDWATFKKHLTDRDWDVDCNLMPTSLF---DCKDKNTFIYSPGVKALCRGVIFSAD 79
QY 59 VLSSTRFQNTCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSNSEFYLAEC---NVKPRKPKCYKLNKSSNRICIRCEHELFVHFAGVGICP 129

RESULT 10
Q9DFY8 PRELIMINARY; PRT; 128 AA.
ID Q9DFY8
AC Q9DFY8
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 4.1e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATVKAICTGVI-NLN 58
Db 24 QNWETFOKKHLTDRDVKDAEMKALF----DCKQNTFIYARPGRVQALCKNIIVSKN 79
QY 59 VLSSTRFQNTCTRTSITPR-PCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 80 VLSTDEFYSDCNRIKL---PCHYKLNKSSNTICITCENKLPVHFVAVEECP 128

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RESULT 5

Q98SM1 PRELIMINARY; PRT; 132 AA.
 ID Q98SM1
 AC Q98SM1; (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNase A-type ribonuclease rc204 precursor.
 OS Rana catesbeiana (bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21593506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, *Rana catesbeiana*.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL; AF351208; AAK30254.1; -.
 DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 74.1%; Score 444.5; DB 13; Length 132;
 Best Local Similarity 77.3%; Pred. No. 2.6e-43;
 Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;
 QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGCKRVNTFISSATVKAICTGVI-NLN 59
 Db 23 QNWTFQKHINTPII-CNTILDNNIYVGGCKRVNTFISSATVKAICTGVI-NLN 59
 QY 60 LSTTRFQKLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 83 LSTTRFQKLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132

RESULT 6

Q9DF78 PRELIMINARY; PRT; 132 AA.
 ID Q9DF78
 AC Q9DF78
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RC-RNaseL1 ribonuclease precursor.
 OS Rana catesbeiana (bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from *Rana*
 RT catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20512555; PubMed=11058105;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from *Rana*
 RT catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF288642; AAG30414.2; -.

DR HSSP; P11916; 1BC4.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 21 POTENTIAL.
 SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
 Query Match 62.0%; Score 372; DB 13; Length 132;
 Best Local Similarity 64.9%; Pred. No. 5.8e-35;
 Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
 QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGCKRVNTFISSATVKAICTGVI-NLN 58
 Db 22 QNWAKPKKHITSTISIDCNTIMDKAIYVGGCKERTFIISSEDNVKAICSGVSPDRK 81
 QY 59 VLSTTRFQKLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 82 ELSTTSFKLNTCTRTSITPRPCPYSPDNKKICVCKEQLPVHFVGIGRC 132

RESULT 7

Q918V8 PRELIMINARY; PRT; 127 AA.
 ID Q918V8
 AC Q918V8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Onconase variant rapRL precursor.
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=20330357; PubMed=10871370;
 RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
 RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
 RT 3' UTR of unusual length and structure.";
 RL Nucleic Acids Res. 28:2375-2382(2000).
 DR EMBL; AF165133; AAF76935.1; -.
 DR PIR; A39035; A39035.
 DR HSSP; P22069; 1ONC.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 23 POTENTIAL.
 SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;
 Query Match 46.2%; Score 277.5; DB 13; Length 127;
 Best Local Similarity 48.6%; Pred. No. 4.2e-24;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
 QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGCKRVNTFISSATVKAICTGVI-NLN 58
 Db 24 QDWLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIIATSKN 79
 QY 59 VLSTTRFQKLTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
 Db 80 VLTTSEFYLSDC---NVTSRCKYKLKSTNTFCVTCENQAPVHFVGHC 127

[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-19

Perfect score: 600

Sequence: 1 QNWATPQQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phase:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	554.5	92.4	133	13	Q98SM0 rana catesb
2	483.5	80.6	132	13	Q98SM2 rana catesb
3	474.5	79.1	133	13	Q98SL9 rana catesb
4	467.5	77.9	133	13	Q98SL8 rana catesb
5	444.5	74.1	132	13	Q98SM1 rana catesb
6	372	62.0	132	13	Q98P78 rana catesb
7	277.5	46.2	127	13	Q98V88 rana pipien
8	273.5	45.6	127	13	Q98VX5 rana pipien
9	243	40.5	129	13	Q98FY6 rana pipien
10	225.5	37.6	128	13	Q98FY8 rana catesb
11	223.5	37.2	128	13	Q98FY7 rana catesb
12	214.5	35.8	128	13	Q98FY5 rana catesb
13	161	26.8	169	13	Q98W78 xenopus lae
14	128	21.3	170	6	Q98EC1 tragus ja
15	127.5	21.2	144	11	Q80Z85 mus musculus
16	127.5	21.2	153	11	Q80XS4 mus musculus

17	123.5	20.6	147	6	Q7YRJ6	Q7YRJ6 balaena mys
18	122	20.3	146	6	Q861Y5	Q861Y5 colobus gue
19	121.5	20.2	116	6	Q9TVC0	Q9TVC0 sus scrofa
20	121.5	20.2	163	6	Q9BDC2	Q9BDC2 antilocapra
21	121	20.2	150	11	Q8VD94	Q8VD94 berylmys bo
22	119	19.8	150	11	Q8VD88	Q8VD88 rattus norv
23	118.5	19.8	144	6	Q9BH14	Q9BH14 antilocapra
24	118.5	19.8	147	6	Q7YRJ5	Q7YRJ5 tursiops tr
25	116.5	19.4	149	11	Q8K2T2	Q8K2T2 mus musculus
26	116.5	19.4	149	11	Q8C6G3	Q8C6G3 mus musculus
27	116	19.3	146	6	Q861Y4	Q861Y4 trachypithe
28	116	19.3	150	11	Q8VD92	Q8VD92 rattus exul
29	115	19.2	146	6	Q861Y3	Q861Y3 pygathrix r
30	115	19.2	146	6	Q861Y2	Q861Y2 pygathrix b
31	115	19.2	146	6	Q861Y1	Q861Y1 pygathrix a
32	113.5	18.9	152	11	Q8VD89	Q8VD89 rattus norv
33	111	18.5	148	11	Q8C6G3	Q8C6G3 mus musculus
34	110.5	18.4	124	6	Q95NE6	Q95NE6 bubalus bub
35	109.5	18.2	148	11	Q8C7E4	Q8C7E4 mus musculus
36	109.5	18.2	149	11	Q8VD95	Q8VD95 berylmys bo
37	109	18.2	124	6	Q9BEC2	Q9BEC2 tragus ja
38	109	18.2	134	6	Q9BDB9	Q9BDB9 tragus tiom
39	108.5	18.1	152	11	Q8VD84	Q8VD84 rattus tiom
40	108.5	18.1	156	6	Q8SQ05	Q8SQ05 lagotherax l
41	107.5	17.9	119	6	Q9TV28	Q9TV28 eulemur ful
42	107.5	17.9	119	6	Q9TV30	Q9TV30 saguinus oe
43	106.5	17.8	156	6	Q8SQ06	Q8SQ06 ateles geof
44	105.5	17.6	142	6	Q9BEC3	Q9BEC3 tragus ja
45	105.5	17.6	156	6	Q8SQ08	Q8SQ08 saimiri sci

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0
AC Q98SM0;
DT 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DE 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCHI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANGREATIC; 1.
KW Signal.
FT SIGNAL. 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 554.5; DB 13; Length 133;

Best Local Similarity 92.8%; Pred. No. 5.6e-56;

Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 QNWATPQQKHINTPII-CNTILDNNIYVGCKKRVNTFIISATTVKAICTGVINLV 59

Db 23 QNWATPQQKHINTPII-CNTILDNNIYVGCKKRVNTFIISATTVKAICTGVINLV 82


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RESULT 11
Q9DFY7 ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242554; AAC31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MM; 2B14986082E0587D CRC64;

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQOKHINT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKKHLDTKKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSTNTITCIVNOLPHIFAGVGSCP 128

Query Match 37.3%; Score 226.5; DB 13; Length 128;
Best Local Similarity 41.1%; Pred. No. 1.6e-18;
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;

QY 2 QNWATFQOKHINT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKKHLDTKKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRAFLPQCDRIKL---PCHYKLSSTNTITCIVNOLPHIFAGVGSCP 128

RESULT 12
Q9DFY5 ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (bullfrog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
DR EMBL; AF242556; AAC31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MM; AFE6FD67D266C7C2 CRC64;

Query Match 35.8%; Score 217.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 1.7e-17;
Matches 44; Conservative 19; Mismatches 40; Indels 9; Gaps 4;

QY 2 QNWATFQOKHINT-PIICNTIMNNIYVGGCKRVNTFISSATVKAICTGV-INNN 59
Db 24 QDMETFKKKHLDTKKVKCDVEMKALF---DCKKNTFIYALPGRVKALCKNIRDNTD 79

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 80 VLSDRVFYLPOCNKKL---PCHYLDGSGNTITCMLKELPHIFAGVGKCP 128

RESULT 13
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PRL2 protein.
GN PRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1] SEQUENCE FROM N.A.
RP MEDLINE=96069863; PubMed=7585965;
RX Kinoshita N., Minshull J., Kirschner M.W.;
RA "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630 (1995).
RN [2] SEQUENCE FROM N.A.
RP Kinoshita N., Kirschner M.W.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF159166; AAD41901.1; -.
DR HSSP; P00656; ILSQ.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MM; D969F3E43BCE1B8 CRC64;

Query Match 26.9%; Score 163; DB 13; Length 169;
Best Local Similarity 39.3%; Pred. No. 5.3e-11;
Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

QY 2 QNWATFQOKHIL--NTPICN-TIMONNIYVGGCKRVNTFI-SSATVKAICTGVIN 57
Db 28 QNINAFMEKHIVKEGAETNCNQTIKORNIRF--KNCKFRNTFTHDNGKKVKEMCAGIVX 86

QY 58 MN-VLSTTRFQNLNCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
Db 87 STFVISEKLLPLTDCLLMGRTAPPCNAYNQITTGVTGTCNNIYVHFAG 138

RESULT 14

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RESULT 8
Q8UVX5      PRELIMINARY;      PRT;      127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL "Rana pipiens onconase genomic DNA.";
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match      45.7%; Score 277.5; DB 13; Length 127;
Best Local Similarity 49.5%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY      2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
Db      24 QDWTFQKKHLTDVDCDNLMTSLF- ---DCKQNTFTIYSLPGPVKALCRGVIFSAD 79
QY      60 VLSTTFQNLNCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db      80 VLTTSEFLSDC- ---NVTSECKYKLLKSTNKFCVTENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6      PRELIMINARY;      PRT;      129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:pancreatic ribonuclease activity; IEA.

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DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN 1 23 POTENTIAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match      40.5%; Score 246; DB 13; Length 129;
Best Local Similarity 43.4%; Pred. No. 8.4e-21;
Matches 49; Conservative 24; Mismatches 30; Indels 10; Gaps 5;

QY      2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
Db      24 QDWTFQKKHLTDVDCDNLMTSLF- ---DCKQNTFTIYSLPGPVKALCRGVIFSAD 79
QY      60 VLSTTFQNLNCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db      80 VLSNSEFVLAEC- ---NVKPRKPKYKLLKSSNRICIRCEHLPVHFAGVIGICP 129

RESULT 10
Q9DFY8      PRELIMINARY;      PRT;      128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
FT CHAIN 1 23 POTENTIAL.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match      37.8%; Score 229.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 7e-19;
Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY      2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFIISATTVAICTGVI-NMN 59
Db      24 QNWETFQKKHLTDVDCDAEMKALF- ---DCKQNTFTIYARPGRVQALCKNIIIVSKN 79
QY      60 VLSTTFQNLNCTRTSITPR-PCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db      80 VLSTDEFYSDCNRIKL- ---PCHYKLLKSSNTTICENKLPVHFVAVEECP 128

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RESULT 5
Q98SM1 PRELIMINARY; PRT; 132 AA.
ID Q98SM1
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 73.9%; Score 448.5; DB 13; Length 132;
Best Local Similarity 78.2%; Pred. No. 2.1e-44;
Matches 86; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 2 QNWATFOQKHINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVIMNV 60
DB 23 QDWPTFOQKHLPSTSSIDCNTIMDKIYVIRGQCKRVNTFISSATTVKAICTGVIMNV 82
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 110
DB 83 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 132

RESULT 6
Q9DF78 PRELIMINARY; PRT; 132 AA.
ID Q9DF78
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11059105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF288642; AAG30414.2; -.

SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11059105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF288642; AAG30414.2; -.

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DR HSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452FBES3 CRC64;

Query Match 61.9%; Score 376; DB 13; Length 132;
Best Local Similarity 65.8%; Pred. No. 5.9e-36;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVIMNV 59
DB 22 QNWAKFKKXHTSTSSIDCNTIMDKIYVIRGQCKRVNTFISSATTVKAICTGVIMNV 81
QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 110
DB 82 ELSTTSFKLNTCTRTSITPRPCPYSPDPNNKICVKCKEQLPVHFVIGKGC 132

RESULT 7
Q918V8 PRELIMINARY; PRT; 127 AA.
ID Q918V8
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapRL precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR HSP; P22069; LONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 46.4%; Score 281.5; DB 13; Length 127;
Best Local Similarity 49.5%; Pred. No. 6e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINTPII-CNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVIMNV 59
DB 24 QDWLTFOQKHINTTRDVCNNIMTNLF---HCKDNFTIYSRPEPVKAICKGLIASKN 79
QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 110
DB 80 VLTTSEFVLSDC---NVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.566 Seconds

(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-17

Perfect score: 607

Sequence: 1 MNWATFOQRKHINTPIICN.....ICVKCENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

1: sp_archaea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phage.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.5	92.3	133	13	Q98SM0 rana catesb
2	487.5	80.3	132	13	Q98SM2 rana catesb
3	478.5	78.8	133	13	Q98SL9 rana catesb
4	471.5	77.7	133	13	Q98SL8 rana catesb
5	448.5	73.9	132	13	Q98SM1 rana catesb
6	376	61.9	132	13	Q9DF78 rana catesb
7	281.5	46.4	127	13	Q918V8 rana pipien
8	277.5	45.7	127	13	Q8UUX5 rana pipien
9	246	40.5	129	13	Q9DFY6 rana pipien
10	229.5	37.8	128	13	Q9DFY8 rana catesb
11	226.5	37.3	128	13	Q9DFY7 rana catesb
12	217.5	35.8	128	13	Q9DFY5 rana catesb
13	163	26.9	169	13	Q9W738 xenopus lae
14	131	21.5	170	6	Q9BEC1 tragulus ja
15	128.5	21.2	144	11	Q80Z85 mus musculus
16	128.5	21.2	153	11	Q80XS4 mus musculus

17	127.5	21.0	147	6	Q7VRJ6	Q7vrj6 balaena mys
18	126	20.8	150	11	Q8VD94	Q8vd94 berylmys bo
19	125.5	20.7	163	6	Q9BDC2	Q9bdc2 antilocapra
20	124.5	20.5	116	6	Q9TVCO	Q9tvco sus scrofa
21	124	20.4	150	11	Q8VD88	Q8vd88 rattus norv
22	122.5	20.2	144	6	Q9BH14	Q9bh14 antilocapra
23	121.5	20.0	147	6	Q7VRJ5	Q7vrj5 tursiops tr
24	121	19.9	146	6	Q861Y5	Q861y5 colobus gue
25	120.5	19.9	149	11	Q8K2T2	Q8k2t2 mus musculu
26	120.5	19.9	149	11	Q8CG63	Q8c6g3 mus musculu
27	120	19.8	150	11	Q8VD92	Q8vd92 rattus exul
28	119.5	19.7	146	6	Q861Y4	Q861y4 trachypithe
29	118.5	19.5	146	6	Q861Y3	Q861y3 pygathrix r
30	118.5	19.5	146	6	Q861Y2	Q861y2 pygathrix b
31	118.5	19.5	146	6	Q861Y1	Q861y1 pygathrix a
32	116.5	19.2	152	11	Q8VD89	Q8vd89 rattus norv
33	114.5	18.9	124	6	Q9SNE6	Q9sne6 bubalus bub
34	112.5	18.5	148	11	Q8C7E4	Q8c7e4 mus musculu
35	112.5	18.5	149	11	Q8VD95	Q8vd95 berylmys bo
36	112	18.5	134	6	Q9BDB9	Q9bdb9 tragulus ja
37	111.5	18.4	152	11	Q8VD84	Q8vd84 rattus tiom
38	111.5	18.4	156	6	Q8SQ05	Q8sq05 lagothrix l
39	111	18.3	148	11	Q8C663	Q8c663 mus musculu
40	110.5	18.2	119	6	Q9TV28	Q9tv28 eulemur ful
41	110.5	18.2	119	6	Q9TV30	Q9tv30 saguinus oe
42	109.5	18.0	142	6	Q9BEC3	Q9bec3 tragulus ja
43	109.5	18.0	156	6	Q8SQ06	Q8sq06 ateles geof
44	109	18.0	124	6	Q9BEC2	Q9bec2 tragulus ja
45	108.5	17.9	156	6	Q8SQ08	Q8sq08 salmirus sci

ALIGNMENTS

RESULT 1

Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TREMREL. 17, Created)
DT 01-JUN-2001 (TREMREL. 17, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.3%; Score 560.5; DB 13; Length 133;
Best Local Similarity 94.6%; Pred. No. 1.8e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Cy 2 QNWATFOQRKHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVINNV 60
Db 23 QNWATFOQRKHINTPII-CNTIMDNNTIYVGQCKRVNTFISSATTVKALCTGVINNV 82

DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; RNaseA; 1.
DR	ProDom; PD000535; RNaseA; 1.
DR	SMART; SM00092; RNase P; 1.
DR	PROSITE; PS00127; RNase_PANCREATIC; 1.
DR	Signal.
FT	SIGNAL. 1 21 POTENTIAL.
FT	CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ	SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
	Query Match 46.5%; Score 270.5; DB 13; Length 132;
	Best Local Similarity 43.6%; Pred. No. 2.4e-23;
	Matches 48; Conservative 19; Mismatches 36; Indels 7; Gaps
QY	3 DMLTQKKHLTNRDVDCNNIMSTNLF----HCKDKNTFIYSRPFPVKAICKGIITASKNV 58
DB	23 NNAKFKKEHITSSIDCNCIMDKAIYIVGGKKERNTFISSDNVKAICSGVSPDRKE 82
QY	59 LTTSEFLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
DB	83 LSTTSEKLTCTRDSITRPPCYHSPDNKKICVCKEQLPVPHFVGVGKC 132
RESULT 13	
Q9W738	PRELIMINARY; PRT; 169 AA.
ID	Q9W738
AC	Q9W738; PRELIMINARY; PRT; 169 AA.
DT	01-NOV-1999 (TREMBlrel. 12, Created)
DT	01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT	01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE	FRL2 protein.
GN	FRL2
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC	Xenopodinae; Xenopus.
OC	NCBI_TaxId=8355;
RP	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=96069863; PubMed=7585965;
EX	Kinoshita N., Minshull J., Kirschner M.W.;
RA	"The identification of two novel ligands of the FGF receptor by a
RT	yeast screening method and their activity in Xenopus development.";
RT	Cell 83:621-630(1995).
RP	[2]
RP	SEQUENCE FROM N.A.
RA	Kinoshita N., Kirschner M.W.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
EMBL	AF159166; AAD41901.1; -.
DR	HSSP; P00656; 1LSQ.
DR	GO; GO:0003676; F:nicotinic acid binding; IEA.
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; RNaseA; 1.
DR	ProDom; PD000535; RNaseA; 1.
DR	PROSITE; PS00127; RNase_PANCREATIC; 1.
SQ	SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;
	Query Match 27.1%; Score 157.5; DB 13; Length 169;
	Best Local Similarity 36.1%; Pred. No. 3.3e-10;
	Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps
QY	7 FQKKHLTNT-RDVDCN-----NIMSTNLFHCKDKNTFIY-SRPFVKAICKGIITASKNV 58
DB	33 FMEKHVKEGATNCNTQTIKDRNIRPKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90
QY	59 LTTSEFLSDCNV---TSRP--CKYKLLKSTNTFCVTCENQAPVHFVG 101
DB	91 ISKELLPLDCLLMGRTAPPNCAYNQRTFTGVINTCENYFVHEAG 138
RESULT 14	


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Db 25 NNETFQKKHLTDTRDVKCAEMKALFDCKQKNTFIYARPRVQALCKNIIVSKNVLSTD 84
QY 63 EYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 EYLSDCNRIKLPCHYKLLKSSNTICITCENKLPVHFVAVEEC 127

RESULT 5
Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT CHAIN
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.6%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.9e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYALFGRVQALCKNIRDNTDVLSD 84
QY 63 EYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 AFLPQCDRIKLPCHYKLLSSNTNICTVCNQLPFIHFAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT CHAIN
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.6%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.9e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYALFGRVQALCKNIRDNTDVLSD 84
QY 63 EYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 AFLPQCDRIKLPCHYKLLSSNTNICTVCNQLPFIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RX Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.3%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 6.1e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db 24 NWATFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYGGQCKGVNTFIISATVKAICTGVI-NMNV 82
QY 59 LATSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

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RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 128 AA; 14804 MW; AFE9FD67D266C7C2 CRC64;

Query Match 52.2%; Score 304; DB 13; Length 128;
Best Local Similarity 53.4%; Pred. No. 3.2e-27;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 3 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYALFGRVQALCKNIRDNTDVLSD 84
QY 63 EYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 VFYLPQNRKKLPCHYRLDGSNTNICTCMKELPIHFAGVGKC 127

RESULT 8
Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RX Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.3%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 6.1e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 3 DMLTFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNV 58
Db 24 NWATFQKKHLTDTRDVCNNIMSTNLFHCKDKNTFIYGGQCKGVNTFIISATVKAICTGVI-NMNV 82
QY 59 LATSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

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Db 25 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 94.7%; Score 551; DB 13; Length 127;
Best Local Similarity 96.1%; Pred. No. 1e-55;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 127

RESULT 3
Q8DFY6 PRELIMINARY; PRT; 129 AA.
AC Q8DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 68.6%; Score 399.5; DB 13; Length 129;
Best Local Similarity 67.3%; Pred. No. 3.1e-38;
Matches 70; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 3 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62
Db 25 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 84
QY 63 EFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 85 EFYLAECNVKPKCKYKLLKSSNRICRCSHELFPVHFAGVGIC 128

RESULT 4
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR PDB; 1M58; 09-JAN-03.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 65.5%; Score 381; DB 13; Length 128;
Best Local Similarity 67.0%; Pred. No. 4.2e-36;
Matches 69; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 3 DWLTFQKKHLINTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTS 62

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds

(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-13

Perfect score: 582

Sequence: 1 MSDWLTFRQKKHLNTRDVC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	98.5	127	13	Q918V8
2	551	94.7	127	13	Q8UVX5
3	399.5	68.6	129	13	Q9DFV6
4	381	65.5	128	13	Q9DFV8
5	306	52.6	128	13	Q9DFV7
6	304	52.2	128	13	Q9DFV5
7	293	50.3	133	13	Q98SM0
8	281	48.3	132	13	Q98SM2
9	281	48.3	133	13	Q98SL9
10	277	47.6	133	13	Q98SL8
11	275	47.3	132	13	Q98SM1
12	270.5	46.5	132	13	Q9DFV8
13	157.5	27.1	169	13	Q9W738
14	133	22.9	152	11	Q9JKI5
15	131	22.5	157	11	Q9JKI9
16	130.5	22.4	153	11	Q9JKI7

17	130	22.3	157	11	Q9JKJ3
18	128.5	22.1	146	6	Q861Y3
19	128.5	22.1	146	6	Q861Y2
20	128.5	22.1	146	6	Q861Y1
21	127	21.8	154	11	Q9JKJ4
22	127	21.8	157	11	Q9JKJ3
23	126	21.6	157	11	Q9JKJ1
24	125	21.5	157	11	Q9JKJ2
25	124.5	21.4	146	6	Q861Y4
26	124.5	21.4	155	11	Q9UKH9
27	123.5	21.2	155	11	Q9UKH3
28	121	20.8	147	6	Q7YRJ6
29	120.5	20.7	155	11	Q9UKI6
30	119.5	20.5	155	11	Q9UKI2
31	119.5	20.5	155	11	Q9UKI4
32	118	20.3	147	6	Q7YRJ5
33	117.5	20.2	155	11	Q9RI34
34	117	20.1	156	11	Q9UKG6
35	117	20.1	156	11	Q9UKH7
36	116.5	20.0	132	6	Q9TV25
37	116.5	20.0	132	6	Q9TV24
38	116.5	20.0	155	11	Q9RI25
39	116.5	20.0	155	11	Q9UKH8
40	116	19.9	156	11	Q9UKG7
41	115	19.8	146	6	Q861Y5
42	115	19.8	156	11	Q9UKH4
43	115	19.8	156	11	Q9UKG9
44	115	19.8	156	11	Q9UKH5
45	114.5	19.7	170	6	Q9BEC1

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMUREL. 15, Created)
DT 01-OCT-2000 (TREMUREL. 15, Last sequence update)
DT 01-OCT-2003 (TREMUREL. 25, Last annotation update)
DE Onconase variant rapRI precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
EX MEDLINE=2030357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -
DR PIR; A39035; A39035.
DR HSP; P22069; 10NC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 98.5%; Score 573; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 3e-58; Indels 0; Gaps 0;
Matches 103; Conservative 0; Mismatches 0;

QY 3 DWLTFQKKHLNTRDVCNINMSTNLFHCKDKNTFYGRPEPVKAICKGIASKNVLTS 62

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O9JKI5
ID Q9JKI5 PRELIMINARY; PRT; 152 AA.
AC Q9JKI5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 10.
CN EAR10.
OS Mus saxicola (Spiny mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10094;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238398; AAF67698.1; -.
DR HSSP; P10153; IHI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PR000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 152 AA; 16830 MW; 780421C3661732C8 CRC64;

Query Match 23.1%; Score 133; DB 11; Length 152;
Best Local Similarity 30.3%; Pred. No. 1.8e-07;
Matches 37; Conservative 19; Mismatches 42; Indels 24; Gaps 6;

Qy 1 SDWLTFOKKHLNTRDVCNNIM---STNLFCKDKNTFYSRPEPKAIC---KGIIA- 53
Db 31 SQW--FATQHTNTANPCNVEMLPINERTCKNINTFLHTFANVVGVCNPSGLCSN 88

Qy 54 --SQNVLTSFYSLDCNVTSR-----PCKYKKKSTNFCVTCENQAP-----VHF 98
Db 89 NISTNCHNSRVPIVCNITREKSKTQCRYQTKGSVEYTVACNPRTPQDSPPYVHL 148

Qy 99 VG 100
Db 149 DG 150

RESULT 15
Q9JKI9
ID Q9JKI9 PRELIMINARY; PRT; 157 AA.
AC Q9JKI9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 44.
CN EAR44.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238394; AAF67694.1; -.
DR HSSP; P10153; IHI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

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DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PR000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EEF3709 CRC64;

Query Match 22.7%; Score 131; DB 11; Length 157;
Best Local Similarity 30.6%; Pred. No. 3.2e-07;
Matches 34; Conservative 20; Mismatches 37; Indels 20; Gaps 7;

Qy 1 SDWLTFOKKHLNTRDVCNNIM---STNLF--HCKDKNTFYSRPEPV-----KAICKG 50
Db 34 SQWFTIQ--HISNTTTICNAAMLGVNNYTGCKDLNLTFLHTFANVNVNRYNNTTCKN 91

Qy 51 IIAKKNVL--TTSEFYSLDCNVTS-----RCKYKKKSTNFCVTCENQAP 95
Db 92 --GRNCHDSRSKVSITDCNLTSPSANYRQCRYQTRARKEYRIACNNKTP 140

Search completed: May 7, 2004, 21:46:02
Job time : 29.5753 secs

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RESULT 14

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      83 LSTTRFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 132
RT      bullfrog, Rana catesbeiana";
RL      J. Mol. Evol. 53:31-38 (2001).
DR      EMBL; AF351210; AAK30253.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
SQ      SEQUENCE 133 AA; 14615 MW; C8785B236B2E54E CRC64;
OX      NCBI_TaxID=8400;
[1]
RN      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RA      Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana.";
RL      J. Mol. Evol. 53:31-38 (2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF351207; AAK30253.1; -.
DR      EMBL; AF359578; AAL87036.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
FT      CHAIN
FT      CHAIN
SQ      SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;
Query Match      48.7%; Score 281; DB 13; Length 132;
Best Local Similarity      47.7%; Pred. No. 1.2e-24;
Matches      52; Conservative      14; Mismatches      35; Indels      8; Gaps      3;
QY      3 WLTFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 58
DB      25 WAKFQKHPTSSINCNTMDNNIYVGGCKKVTFISSATVKAICNG-VTNSNV 83
QY      59 TTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB      84 SPTRFQDLTCTRTSITPRPCPYSSKKTNTKICVRCENQLPVHFAGIGKC 132
RESULT 9
Q98SL9
ID      Q98SL9      PRELIMINARY;      PRT;      133 AA.
AC      Q98SL9;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX      NCBI_TaxID=8400;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RA      Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana.";
RL      J. Mol. Evol. 53:31-38 (2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF351207; AAK30253.1; -.
DR      EMBL; AF359578; AAL87036.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
FT      CHAIN
FT      CHAIN
SQ      SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;
Query Match      48.7%; Score 281; DB 13; Length 132;
Best Local Similarity      47.7%; Pred. No. 1.2e-24;
Matches      52; Conservative      14; Mismatches      35; Indels      8; Gaps      3;
QY      3 WLTFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 58
DB      25 WAKFQKHPTSSINCNTMDNNIYVGGCKKVTFISSATVKAICNG-VTNSNV 83
QY      59 TTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB      84 SPTRFQDLTCTRTSITPRPCPYSSKKTNTKICVRCENQLPVHFAGIGKC 132
RESULT 9
Q98SL9
ID      Q98SL9      PRELIMINARY;      PRT;      133 AA.
AC      Q98SL9;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RNase A-type ribonuclease rc212 precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX      NCBI_TaxID=8400;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RA      Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana.";
RL      J. Mol. Evol. 53:31-38 (2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL      Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF351207; AAK30253.1; -.
DR      EMBL; AF359578; AAL87036.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
FT      CHAIN
FT      CHAIN
SQ      SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
Query Match      48.0%; Score 277; DB 13; Length 133;
Best Local Similarity      46.4%; Pred. No. 3.6e-24;
Matches      51; Conservative      18; Mismatches      33; Indels      8; Gaps      3;
QY      2 DMLTFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 57
DB      24 NMAIFQKHITNTSSINCNMNNSLYIVGGCKKVTFIASSATVKGICSG-VTDKKV 82
QY      58 LTTSEFYLSDCN---VTSRCPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB      83 LSSTKFQDLICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132

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RT      bullfrog, Rana catesbeiana";
RL      J. Mol. Evol. 53:31-38 (2001).
DR      EMBL; AF351210; AAK30256.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
SQ      SEQUENCE 133 AA; 14615 MW; C8785B236B2E54E CRC64;
Query Match      48.7%; Score 281; DB 13; Length 133;
Best Local Similarity      47.3%; Pred. No. 1.2e-24;
Matches      52; Conservative      17; Mismatches      33; Indels      8; Gaps      3;
QY      2 DMLTFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 57
DB      24 NMAIFQKHITNTSSINCNMNNSLYIVGGCKKVTFIASSATVKGICSG-VTDKKV 82
QY      58 LTTSEFYLSDCN---VTSRCPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB      83 LSSTKFQDLICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132

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RESULT 10
Q98SL8
ID      Q98SL8      PRELIMINARY;      PRT;      133 AA.
AC      Q98SL8;
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RNase A-type ribonuclease rc218 precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX      NCBI_TaxID=8400;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21539506; PubMed=11683320;
RA      Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT      "Rapid diversification of RNase A superfamily ribonuclease from the
RT      bullfrog, Rana catesbeiana.";
RL      J. Mol. Evol. 53:31-38 (2001).
DR      EMBL; AF351211; AAK30257.1; -.
DR      HSSP; P11916; 1BC4.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF00074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
SQ      SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
Query Match      48.0%; Score 277; DB 13; Length 133;
Best Local Similarity      46.4%; Pred. No. 3.6e-24;
Matches      51; Conservative      18; Mismatches      33; Indels      8; Gaps      3;
QY      2 DMLTFQKHLNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKNV 57
DB      24 NMAIFQKHITNTSSINCNMNNSLYIVGGCKKVTFIASSATVKGICSG-VTDKKV 82
QY      58 LTTSEFYLSDCN---VTSRCPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB      83 LSSTKFQDLICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132

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Db 25 NMEFTQKKHLTDTRDKVCKDAEMKALFDCKQKNTFIYARPRVOALCKNIIVSKNVLSTD 84
QY 62 EFLVSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 EFLVSDCNRIKLPCHYKLLKSSNTICITCENKLPVHFVAVEEC 127

RESULT 5
Q9DFY7 PRELIMINARY; PRT; 128 AA.
ID Q9DFY7
AC Q9DFY7;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.5e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETQKKHLTDTRDKVCKDVMKALFDCKKNTFIYALPGRVKALCKNIRDNDVLSD 84

QY 62 EFLVSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 AFLPQCDRIKLPCHYKLLSSTNTICITCVNQLPIHFAGVGC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
ID Q9DFY5
AC Q9DFY5;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 54.4%; Pred. No. 1.5e-27;
Matches 56; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETQKKHLTDTRDKVCKDVMKALFDCKKNTFIYALPGRVKALCKNIRDNDVLSD 84

QY 62 EFLVSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 AFLPQCDRIKLPCHYKLLSSTNTICITCVNQLPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0
AC Q98SM0;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.8%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 5e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKN 57
Db 24 NWATFQKKHLTNTSINCNTINDNNIYVGGCKGVNTFISSATVKAICTGVI-MNV 82
QY 58 LTTSEFYISDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
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RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 52.7%; Score 304; DB 13; Length 128;
Best Local Similarity 53.4%; Pred. No. 2.6e-27;
Matches 55; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLTS 61
Db 25 DWETQKKHLTDTRDKVCKDVMKALFDCKKNTFIYALPGRVKALCKNIRDNDVLSD 84

QY 62 EFLVSDCNVTSRCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 85 VFYLPQCNRRKKLPCHYLDGSGTNTICITCMKELPIHFAGVGC 127

RESULT 7
Q98SM0 PRELIMINARY; PRT; 133 AA.
ID Q98SM0
AC Q98SM0;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 50.8%; Score 293; DB 13; Length 133;
Best Local Similarity 49.1%; Pred. No. 5e-26;
Matches 54; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 2 DMLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKN 57
Db 24 NWATFQKKHLTNTSINCNTINDNNIYVGGCKGVNTFISSATVKAICTGVI-MNV 82
QY 58 LTTSEFYISDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
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Db 25 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 84
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 104
Db 85 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 127

RESULT 2
Q8UVX5
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TremBLrel. 20, Created)
DT 01-MAR-2002 (TremBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Onconase precursor.
GS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PG; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 127 AA; 14469 MW; 95390D351CFEEF3 CRC64;

Query Match 95.5%; Score 551; DB 13; Length 127;
Best Local Similarity 96.1%; Pred. No. 7.1e-56;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 61
Db 25 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 84
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 104
Db 85 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 127

RESULT 3
Q9DFY6
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-OCT-2001 (TremBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

QY 2 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 61
Db 25 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 84
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 104
Db 85 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 127

RESULT 4
Q9DFY8
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

QY 2 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 61
Db 25 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 84
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 104
Db 85 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 127

Query Match 69.2%; Score 399.5; DB 13; Length 129;
Best Local Similarity 67.3%; Pred. No. 2.4e-38;
Matches 70; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 61
Db 25 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 84
QY 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 104
Db 85 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGVC 127

Query Match 66.0%; Score 381; DB 13; Length 128;
Best Local Similarity 67.0%; Pred. No. 3.2e-36;
Matches 69; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 DWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLTTS 61

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-11
Perfect score: 577
Sequence: 1 SDWLTFQKXHLNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 31518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_ivirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	99.3	127	13 Q818V8	Q818v8 rana pipien
2	551	95.5	127	13 Q8UVX5	Q8uvx5 rana pipien
3	399.5	69.2	129	13 Q9DFY6	Q9dfy6 rana catesb
4	381	66.0	128	13 Q9DFY8	Q9dfy8 rana catesb
5	306	53.0	128	13 Q9DFY7	Q9dfy7 rana catesb
6	304	52.7	128	13 Q9DFY5	Q9dfy5 rana catesb
7	293	50.8	133	13 Q98SM0	Q98sm0 rana catesb
8	281	48.7	132	13 Q98SL9	Q98sl9 rana catesb
9	281	48.7	133	13 Q98SL8	Q98sl8 rana catesb
10	277	48.0	133	13 Q98SM1	Q98sm1 rana catesb
11	275	47.7	132	13 Q98FM1	Q98fm1 rana catesb
12	270.5	46.9	132	13 Q9DF78	Q9df78 rana catesb
13	157.5	27.3	169	13 Q9W738	Q9w738 xenopus lae
14	133	23.1	152	11 Q9JKI5	Q9jki5 mus saxicol
15	131	22.7	157	11 Q9UK19	Q9juk19 meriones un
16	130.5	22.6	153	11 Q9JKI7	Q9jki7 mus saxicol

17	130	22.5	157	11 Q9UKJ3	Q9jukj3 meriones un
18	128.5	22.3	146	6 Q861V3	Q861v3 pygathrix r
19	128.5	22.3	146	6 Q861V2	Q861v2 pygathrix b
20	128.5	22.3	146	6 Q861V1	Q861v1 pygathrix a
21	127	22.0	154	11 Q9UKI8	Q9juk18 mus saxicol
22	127	22.0	157	11 Q9UKJ4	Q9jukj4 meriones un
23	126	21.8	157	11 Q9UKJ1	Q9jukj1 meriones un
24	125	21.7	157	11 Q9UKJ2	Q861v4 trachypithe
25	124.5	21.6	146	6 Q861V4	Q9jkh9 mus pahari
26	124.5	21.6	155	11 Q9UKH9	Q9jki3 mus saxicol
27	123.5	21.4	155	11 Q9UKI3	Q9yri6 balaena mys
28	121	21.0	147	6 Q7YR36	Q9jki6 mus saxicol
29	120.5	20.9	155	11 Q9UKI6	Q9jki2 mus saxicol
30	119.5	20.7	155	11 Q9UKI2	Q9jki4 mus saxicol
31	119.5	20.7	155	11 Q9UKI4	Q9yri5 tursiops tr
32	118	20.5	147	6 Q7YR35	Q9yri3 rattus norv
33	117.5	20.4	155	11 Q9UKI34	Q9jkg6 mus caroli
34	117	20.3	155	11 Q9UKG6	Q9jkh7 mus caroli
35	117	20.3	156	11 Q9UKH7	Q9tv25 eulemur ful
36	116.5	20.2	132	6 Q9TV25	Q9r125 mus musculu
37	116.5	20.2	155	11 Q9UKI25	Q9jkh8 mus pahari
38	116.5	20.2	155	11 Q9UKH8	Q9jkg7 mus caroli
39	116	20.1	156	11 Q9UKG7	Q8ei5 colobus gue
40	115	19.9	146	6 Q861V5	Q9jkh4 mus caroli
41	115	19.9	156	11 Q9UKH4	Q9jkg9 mus caroli
42	115	19.9	156	11 Q9UKG9	Q9jkh5 mus caroli
43	115	19.9	156	11 Q9UKH5	Q9tv24 galago moho
44	114.5	19.8	132	6 Q9TV24	Q9bec1 tragulus ja
45	114.5	19.8	170	6 Q9BEC1	

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.
ID Q918V8;
AC Q918V8;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Onconase variant rap1R1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -
DR PIR; A39035; A39035.
DR HSSB; P22069; LONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.3%; Score 573; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DMLTFQKXHLNTRDVDCNINMSTNLFHCKDKNTFYSRPEPVKAICKGLIASKNVLTTS 61

RESULT 11	
Q98SM1	PRELIMINARY; PRT; 132 AA.
AC	Q98SM1;
DT	01-JUN-2001 (TrEMBLrel. 17, Created)
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	RNase A-type ribonuclease rc204 precursor.
OS	Rana catesbeiana (Bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=21539506; PubMed=11683320;
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT	"rapid diversification of RNase A superfamily ribonuclease from the
RT	bullfrog, Rana catesbeiana."
RL	J. Mol. Evol. 53:31-38 (2001).
DR	HSSP; P11916; 1BC4.
DR	GO: 0003676; F:nucleic acid binding; IEA.
DR	GO: 0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; RNaseA; 1.
DR	ProDom: PD000535; RNaseA; 1.
DR	SMART: SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR	Signal.
KW	SIGNAL.
FT	CHAIN 1 21 POTENTIAL.
SQ	SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
Query Match 46.2%; Score 270; DB 13; Length 132;	
Best Local Similarity 47.7%; Pred. No. 1.7e-23;	
Matches 53; Conservative 13; Mismatches 37; Indels 8; Gaps 3;	
QY 2 QDWLTFQKKHLNTRDVCNNILSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 57	
DB 23 QDWTFQKKHLPSTSSIDCNTIMDKIYIVRGQCKKVNFTIYSATTVKAICTGVLSN-N 81	
QY 58 VLTTTFEFLSDCN--ATSRPCKYKLLKSTNTFCVTENQAPVHFVGVGHC 105	
DB 82 VLSTTRFQLXXXTRFTITSRCPYSSYKTNKICVKCENEYVHFAGIGKC 132	
RESULT 12	
Q9DF78	PRELIMINARY; PRT; 132 AA.
AC	Q9DF78;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	RC-RNaseL1 ribonuclease precursor.
OS	Rana catesbeiana (Bull frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX	NCBI_TaxID=8400;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=20512555; PubMed=11058105;
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT	"Purification and cloning of cytotoxic ribonucleases from Rana
RT	catesbeiana (bullfrog)."
RL	Nucleic Acids Res. 28:4097-4104 (2000).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Liver;
RX	MEDLINE=20512555; PubMed=11058105;
RA	Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF288642; AAG30414.2; -
DR	HSSP; P11916; 1BC4.
DR	GO: 0003676; F:nucleic acid binding; IEA.

RESULT 13	
Q9W738	PRELIMINARY; PRT; 169 AA.
ID	Q9W738
AC	Q9W738;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	FRL2 protein.
GN	FRL2.
OS	Xenopus laevis (African clawed frog).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC	Xenopodinae; Xenopus.
NCBI_TaxID=8355;	
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=96069663; PubMed=7585965;
RA	Kinoshita N., Minshall J., Kirschner M.W.;
RT	"The identification of two novel ligands of the FGF receptor by a
RT	yeast screening method and their activity in Xenopus development."
RL	Cell 83:621-630 (1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Kinoshita N., Kirschner M.W.;
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AF159166; AAD41901.1; -
DR	HSSP; P06566; 1LSQ.
DR	GO: 0003676; F:nucleic acid binding; IEA.
DR	GO: 0004522; F:pancreatic ribonuclease activity; IEA.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF00074; RNaseA; 1.
DR	ProDom: PD000535; RNaseA; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ	SEQUENCE 169 AA; 18831 MW; D969F3E43B3CE1B8 CRC64;
Query Match 26.5%; Score 154.5; DB 13; Length 169;	
Best Local Similarity 36.1%; Pred. No. 5.7e-10;	
Matches 39; Conservative 18; Mismatches 36; Indels 15; Gaps 6;	
QY 7 FQKHLNTRDVCN-----NILSTNLHCKDKNTFIYSRPEPVKAICKGIIASKN 58	
DB 33 FMEKHIVKEGATNCNQTIKDRNIRFKN--NCKFRNTFHDTNGKKVKEMCAGIVKSTFV 90	
QY 59 LTTTFEFLSDC---NATSRP--CKYKLLKSTNTFCVTENQAPVHFVG 101	
DB 91 ISKELLPLTDCLLMGRTARPPNCAYNQTRTGTGVIITCENNYPVHFAG 138	
RESULT 14	

RT	bullfrog, Rana catesbeiana."	
RL	J. Mol. Evol. 53:31-38(2001).	
DR	EMBL; AF351210; AAK30256.1; -.	
DR	HSSP; P11916; 1BC4.	
DR	GO; GO:0003676; F:nucleic acid binding; IEA.	
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.	
DR	InterPro; IPR001427; RNaseA.	
DR	Pfam; PF00074; rnaseA; 1.	
DR	ProDom; PD000535; RNaseA; 1.	
DR	SMART; SM00092; RNase_Pc; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
KW	Signal.	
FT	SIGNAL.	
SEQ	SEQUENCE 133 AA; 14615 MW; C8785B23626E54E CRC64;	
	Query Match 47.3%; Score 276; DB 13; Length 133;	
	Best Local Similarity 45.9%; Pred. No. 3.4e-24;	
	Matches 52; Conservative 16; Mismatches 35; Indels 8; Gaps 3;	
QY	2 QDWLTFOKKHLTNTRDVCNNILSTNLF---HCKDKNTFTYSRPEPVKAICKGIIASKN 57	
Db	23 QNWATFOQKHITNTSSINCNSIMNNSLYIVGGQCKVNTFIASATTVKICSG-VTDKK 81	
QY	58 VLTTFEYFLSDCN---ATSPCKYKLKKSTNTFCVTCENQAPVHFVGHC 105	
Db	82 VLSSTKFDLICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132	
RESULT 10		
Q98SL8	PRELIMINARY; PRT; 133 AA.	
ID	Q98SL8	
AC	Q98SL8;	
DT	01-JUN-2001 (TrEMBLrel. 17, Created)	
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)	
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
DE	RNase A-type ribonuclease rc218 precursor.	
OS	Rana catesbeiana (Bull frog).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.	
OX	NCBI_TaxID=8400;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=21539506; PubMed=11683320;	
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;	
RT	"Rapid diversification of Rana A superfamily ribonuclease from the	
RT	bullfrog, Rana catesbeiana."	
EL	J. Mol. Evol. 53:31-38(2001).	
DR	EMBL; AF351211; AAK30257.1; -.	
DR	HSSP; P11916; 1BC4.	
DR	GO; GO:0003676; F:nucleic acid binding; IEA.	
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.	
DR	InterPro; IPR001427; RNaseA.	
DR	Pfam; PF00074; rnaseA; 1.	
DR	ProDom; PD000535; RNaseA; 1.	
DR	SMART; SM00092; RNase_Pc; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
KW	Signal.	
FT	SIGNAL.	
SEQ	SEQUENCE 133 AA; 14590 MW; 8B40B9A94FASB943 CRC64;	
	Query Match 46.6%; Score 272; DB 13; Length 133;	
	Best Local Similarity 45.9%; Pred. No. 9.9e-24;	
	Matches 51; Conservative 17; Mismatches 35; Indels 8; Gaps 3;	
QY	2 QDWLTFOKKHLTNTRDVCNNILSTNLF---HCKDKNTFTYSRPEPVKAICKGIIASKN 57	
Db	23 QNWATFOQKHITNTSSINCNSIMNNSLYIVGGQCKVNTFIASATTVKICSG-VTDKK 81	
QY	58 VLTTFEYFLSDCN---ATSPCKYKLKKSTNTFCVTCENQAPVHFVGHC 105	
Db	82 VLSSTKFDLICTRIFITPRPCPYSSRTETNYICVKCENQYPVHFAGIGQC 132	

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Db 24 QNWTFQKHLTDTRVCKDAEMKALFDCKQKNTFIYARPGRVQALCKNIIVKSNVLT 83
QY 62 FEFYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105
Db 84 DEFYLSDCNRKLPCHYKLLKSSNTTICENKPLVHFVAVEEC 127

RESULT 5
Q9DFY7
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-WAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;
RP TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
   catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.6%; Score 307; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 8.2e-28;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNTDRVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 24 QDWTFQKHLTDTRVCKDAEMKALFDCKQKNTFIYALPGRVKALCKNIRDNTVLSR 83
QY 62 FEFYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105
Db 84 DAFLLPQCDRIKLPCHYKLLKSSNTTICITCVNQLPIHFAGVGC 127

RESULT 6
Q9DFY5
ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-WAR-2001 (Tremblrel. 16, Created)
DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
   catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.6%; Score 307; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 8.2e-28;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNTDRVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 24 QDWTFQKHLTDTRVCKDAEMKALFDCKQKNTFIYALPGRVKALCKNIRDNTVLSR 83
QY 62 FEFYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105
Db 84 DAFLLPQCDRIKLPCHYKLLKSSNTTICITCVNQLPIHFAGVGC 127

RESULT 7
Q98SMO
ID Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
   bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.0%; Score 292; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 4.7e-26;
Matches 55; Conservative 14; Mismatches 34; Indels 8; Gaps 3;

QY 2 QDWLTFQKHLTNTDRVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 23 QNWTFQKHLTNTSSINCNTIMDNITVIGVQCKGVNTFISSATTVAICTGVI-NNN 81
QY 58 VLTTFEYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105

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RL Nucleic Acids Res. 28:4097-4104(2000).
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -.
DR HSSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFD67D266C7C2 CRC64;

Query Match 52.2%; Score 305; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 1.4e-27;
Matches 55; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNTDRVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 24 QDWTFQKHLTDTRVCKDAEMKALFDCKQKNTFIYALPGRVKALCKNIRDNTVLSR 83
QY 62 FEFYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105
Db 84 DVFYLPQCNRRKLPCHYRLDGSNTTICLTKMKELPIHFAGVGC 127

RESULT 7
Q98SMO
ID Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN SEQUENCE FROM N.A.
RP MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
   bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; IBC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;
SQ SEQUENCE 133 AA; 14628 MW; 87FCF12C3499E02 CRC64;

Query Match 50.0%; Score 292; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 4.7e-26;
Matches 55; Conservative 14; Mismatches 34; Indels 8; Gaps 3;

QY 2 QDWLTFQKHLTNTDRVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGLIASKNVLT 61
Db 23 QNWTFQKHLTNTSSINCNTIMDNITVIGVQCKGVNTFISSATTVAICTGVI-NNN 81
QY 58 VLTTFEYLSDCNATSRPCPKYKLLKSNTEFCVTENQAPVHFVGVGHC 105

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-8

Perfect score: 584

Sequence: 1 MQDWLTFQKKHLTNRDVC.....TFCVTCENQAPVHVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPREMBL_25.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp Vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	565	96.7	127	13	Q918V8
2	543	93.0	127	13	Q8UVX5
3	391.5	67.0	129	13	Q9DFV6
4	382	65.4	128	13	Q9DFY8
5	307	52.6	128	13	Q9DFY7
6	305	52.2	128	13	Q9DFY5
7	292	50.0	133	13	Q98SM0
8	279	47.8	132	13	Q98SM2
9	276	47.3	133	13	Q98SL9
10	272	46.6	133	13	Q98SL8
11	270	46.2	132	13	Q98SM1
12	265.5	45.5	132	13	Q9DF78
13	154.5	26.5	169	13	Q9W738
14	120	20.5	157	11	Q9JKJ3
15	120	20.5	157	11	Q9JKI9
16	119.5	20.5	146	6	Q86LY3

17	119.5	20.5	146	6	Q86LY2
18	119.5	20.5	146	6	Q86LY1
19	118	20.2	157	11	Q9UKJ4
20	117	20.0	157	11	Q9UKJ2
21	116	19.9	152	11	Q9UKI5
22	115.5	19.8	153	11	Q9UKI7
23	115	19.7	147	6	Q7YRJ5
24	115	19.7	157	11	Q9UKJ1
25	114.5	19.6	146	6	Q86LY4
26	113.5	19.4	132	6	Q9TV24
27	113	19.3	147	6	Q7YRJ6
28	111.5	19.1	119	6	Q9TSQ6
29	111.5	19.1	119	6	Q9TV32
30	111.5	19.1	147	6	Q8HZQ0
31	110.5	18.9	119	6	Q9TV30
32	110	18.8	154	11	Q9UKI8
33	109.5	18.8	155	11	Q9UKH9
34	108.5	18.6	132	6	Q9TV25
35	108.5	18.6	155	11	Q9UKI3
36	108	18.5	124	6	Q95NE6
37	108	18.5	146	6	Q86LY5
38	106.5	18.2	155	11	Q9UKH8
39	106.5	18.2	170	6	Q9BEC1
40	106	18.2	144	6	Q9BH14
41	105.5	18.1	144	11	Q80Z85
42	105.5	18.1	153	11	Q80XS4
43	105.5	18.1	155	11	Q9UKI6
44	104.5	17.9	119	6	Q9TV31
45	104.5	17.9	155	11	Q9UKI2

ALIGNMENTS

RESULT 1

ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Onconase variant rap1 precursor
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
EX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165113; AAF76935.1; -
DR PIR; A39035; A39035.
DR HSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00032; RNase_Fc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 1 23 POTENTIAL.
SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 96.7%; Score 565; DB 13; Length 127;
Best Local Similarity 97.1%; Pred. No. 8.7e-58;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFYSRPEPKAICKGLIASKNVLT 61


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Q861Y3
ID Q861Y3 PRELIMINARY; PRT; 146 AA.
AC Q861Y3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Angiogenin.
OS Pygathrix roxellana (golden snub-nosed monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61622;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22597544; PubMed=12711394;
RA Zhang J., Zhang Y.-P.;
RT "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT eating monkey.";
RL Gene 308:95-101(2003).
DR EMBL; AY221130; AAC41337.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;

Query Match 22.2%; Score 129.5; DB 6; Length 146;
Best Local Similarity 34.2%; Pred. No. 4.2e-07;
Matches 38; Conservative 16; Mismatches 40; Indels 17; Gaps 7;

QY 2 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
DB 31 RDFLT---KHYDATPQGRNDRYCESMRRRGITSPCKDINTFIHGNRSRIKAICGDENG 87
QY 53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLLKSTNTFCVTCENQAPVH 98
DB 88 PYGENLRISKSPFQVTTCTNLRGSSRPPCRVATAGFRNIVVACENDLPVH 138

RESULT 15
Q861Y2
ID Q861Y2 PRELIMINARY; PRT; 146 AA.
AC Q861Y2;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Angiogenin.
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
OC Pygathrix.
OX NCBI_TaxID=61621;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22597544; PubMed=12711394;
RA Zhang J., Zhang Y.-P.;
RT "Pseudogenization of the tumor-growth promoter angiogenin in a leaf-
RT eating monkey.";
RL Gene 308:95-101(2003).
DR EMBL; AY221131; AAC41338.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 146 AA; 16438 MW; 8CF170A4BD12BA67 CRC64;
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Query Match 22.2%; Score 129.5; DB 6; Length 146;
Best Local Similarity 34.2%; Pred. No. 4.2e-07;
Matches 38; Conservative 16; Mismatches 40; Indels 17; Gaps 7;

QY 2 QDWLTFQKKHLTNT----RDVDCNNIMSTN--LFHCKDKNTFIYSRPEPVKAIC---KGI 52
DB 31 RDFLT---KHYDATPQGRNDRYCESMRRRGITSPCKDINTFIHGNRSRIKAICGDENG 87
QY 53 IASKNV-LTTSEFYLSDCNV---TSR-PCKYKLLKSTNTFCVTCENQAPVH 98
DB 88 PYGENLRISKSPFQVTTCTNLRGSSRPPCRVATAGFRNIVVACENDLPVH 138

Search completed: May 7, 2004, 21:46:01
Job time : 29.8597 secs
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RESULT 11

Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
bullfrog, Rana catesbeiana";
RL J. Mol. Evol. 53:31-38 (2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 48.0%; Score 280; DB 13; Length 132;
Best Local Similarity 48.6%; Pred. No. 1.4e-24;
Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;
QY 2 QDWLTFQKHLTNTDVCNNIMTNLF-----HCKDKNTFIYSRPEPVKAICKGIASKN 57
Db 23 QDWPTFQKHPSTSSIDCNTIMDKDIYIVRGCKKVNFTFIYSATTVKAICTGVLSN-N 81
QY 58 VLTTSFYLSDCN----VTSRPCKYKLKSTNTFCVTCNQAPVHFVGVGHC 105
Db 82 VLSTTRFQLXXXTRFTTSRCPYSGSTKRTNKICKVCNEVYVHPAGIGKC 132

RESULT 12

Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14695 MW; D8D9A517452FBE53 CRC64;

Query Match 47.3%; Score 275.5; DB 13; Length 132;
Best Local Similarity 44.1%; Pred. No. 4.6e-24;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;
QY 2 QDWLTFQKHLTNTDVCNNIMTNLF-----HCKDKNTFIYSRPEPVKAICKGIASKN 57
Db 22 QWAXFKEKHITSTSSIDCNTIMDKAIYIVGCKKERNTFIISSEDNVKAICGVSPPDRK 81
QY 58 VLTTSFYLSDC---NVTSRPCKYKLKSTNTFCVTCNQAPVHFVGVGHC 105
Db 82 ELSTTSFKLNTCIRDSITPRPCYPHSPDNNKICVACEKQLPVPVFGIGKC 132

RESULT 13

Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1; -.
DR HSP; P00656; 1LSQ.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match 27.0%; Score 157.5; DB 13; Length 169;
Best Local Similarity 36.1%; Pred. No. 2.8e-10;
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;
QY 7 FQKHLTNT-RDVCN-----NIMSTNLFFCKDKNTFIY-SRPEPVKAICKGIASKN 58
Db 33 FMEKHIVKEGAETNCNQTKDRNIRFKN--NCKFRNTFIHDTNGKVKKEMCAGIVKSTFV 90
QY 59 LTTSEFYLSDCNV---TSRP--CKYKLKSTNTFCVTCNQAPVHFVG 101
Db 91 ISKELLPLTDLGMRTARPENCAYNQTRTGVINICENNYVPHFAG 138

RESULT 14

Db 24 QNWETFOKKHLTDRDVKDAEMKALPDKCKQNTFIYARPGVQALCKNIIVKXNVLST 83

Qy 62 SEFYLSDCNVTSRPCYKYLKSTNTFCVTCENQAPVHFVGVGHC 105

Db 84 DEFYLSDCNRIKLPCHYKLSNSTICITCENKLPVHFVAVBEC 127

RESULT 5

Q9DFY7

ID Q9DFY7 PRELIMINARY; PRT; 128 AA.

AC 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE RC-RNase3 ribonuclease precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=20512555; PubMed=11058105;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";

RL Nucleic Acids Res. 28:4097-4104(2000).

DR EMBL; AF242554; AAG31440.2; -.

DR HSSP; P22069; 10NC.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnasea; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

KW SIGNAL.

FT CHAIN 1 23 POTENTIAL.

FT CHAIN 24 128 RC-RNase3 RIBONUCLEASE.

SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.3%; Score 311; DB 13; Length 128;

Best Local Similarity 54.8%; Pred. No. 3.5e-28;

Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

Qy 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

Db 24 QDWLTFQKKHLTDTKKVKCDVEMAKALFDCKTNTFIYALPGRVKALCKNIRDNTDVLNR 83

Qy 62 SEFYLSDCNVTSRPCYKYLKSTNTFCVTCENQAPVHFVGVGHC 105

Db 84 DAFLPQCDRIKLPCHYKLSNSTICITCENQALPFIHFAGVGC 127

RESULT 6

Q9DFY5

ID Q9DFY5 PRELIMINARY; PRT; 128 AA.

AC 01-MAR-2001 (TREMELrel. 16, Created)

DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE RC-RNase6 ribonuclease precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA MEDLINE=20512555; PubMed=11058105;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";

RL Nucleic Acids Res. 28:4097-4104(2000).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF242556; AAG31442.2; -.

DR HSSP; P22069; 10NC.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnasea; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

KW SIGNAL.

FT CHAIN 1 23 POTENTIAL.

FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.

SQ SEQUENCE 128 AA; 14804 MW; AFE6FD67D266C7C2 CRC64;

Query Match 53.0%; Score 309; DB 13; Length 128;

Best Local Similarity 53.8%; Pred. No. 5.9e-28;

Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

Qy 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

Db 24 QDWLTFQKKHLTDTKKVKCDVEMKALFDCKTNTFIYARPFVQALCKNIKIDNTNVLNR 83

Qy 62 SEFYLSDCNVTSRPCYKYLKSTNTFCVTCENQAPVHFVGVGHC 105

Db 84 DVFYLPQCNRRKKLPCHYRLDGSNTICITCMKELPIHFAGVGKC 127

RESULT 7

Q98SMO

ID Q98SMO PRELIMINARY; PRT; 133 AA.

AC Q98SMO;

DT 01-JUN-2001 (TREMELrel. 17, Created)

DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE RNase A-type ribonuclease rc208 precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=21539506; PubMed=11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the bullfrog, Rana catesbeiana";

RL J. Mol. Evol. 53:31-38(2001).

DR EMBL; AF351209; AAK30255.1; -.

DR HSSP; P11916; 1BC4.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; rnasea; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_PC; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

DR SIGNAL.

FT CHAIN 1 22 POTENTIAL.

SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.1%; Score 298; DB 13; Length 133;

Best Local Similarity 49.5%; Pred. No. 1.2e-26;

Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

Qy 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Db 23 QNWATFOKKHLTNTSSINCNTIMDNNTIYVGGQCKGVNTFISSATTCAICTGYI--NMN 81

Qy 58 VLTITSEFYLSDC--NVTSPCKYKYLKSTNTFCVTCENQAPVHFVGVGHC 105

```

Db 24 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CPEEF3 CRC64;

Query Match 95.4%; Score 556; DB 13; Length 127;
Best Local Similarity 96.2%; Pred. No. 1.4e-56;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db 24 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]

Query Match 66.2%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 7.1e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

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RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.
SQ SEQUENCE 129 AA; 14724 MW; 826AG62892B10ABDA CRC64;

Query Match 69.4%; Score 404.5; DB 13; Length 129;
Best Local Similarity 67.6%; Pred. No. 5.1e-39;
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61
Db 24 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 83
QY 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 128

RESULT 4
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCB1_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]

Query Match 66.2%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 7.1e-37;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNTDRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTT 61

```

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.8597 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-6
Perfect score: 583
Sequence: 1 MQDWLTFFQKHLTNRDVC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 25:.*
1: sp_archaea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phase:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertebrate:.*
14: sp_unclassified:.*
15: sp_rvirus:.*
16: sp_bacteriap:.*
17: sp_archaeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	578	99.1	127	13 Q918V8	Q918V8 rana pipien
2	556	95.4	127	13 Q8UVX5	Q8UVX5 rana pipien
3	404.5	69.4	129	13 Q9DFY6	Q9DFY6 rana catesb
4	386	66.2	128	13 Q9DFY8	Q9DFY8 rana catesb
5	311	53.3	128	13 Q9DFY7	Q9DFY7 rana catesb
6	309	53.0	128	13 Q9DFY5	Q9DFY5 rana catesb
7	298	51.1	133	13 Q98SM0	Q98SM0 rana catesb
8	286	49.1	133	13 Q98SL9	Q98SL9 rana catesb
9	285	48.9	132	13 Q98SM2	Q98SM2 rana catesb
10	282	48.4	132	13 Q98SL8	Q98SL8 rana catesb
11	280	48.0	132	13 Q98SLM1	Q98SLM1 rana catesb
12	275.5	47.3	132	13 Q9DF78	Q9DF78 rana catesb
13	157.5	27.0	169	13 Q9W738	Q9W738 xenopus lae
14	129.5	22.2	146	6 Q861Y3	Q861Y3 pygathrix a
15	129.5	22.2	146	6 Q861Y2	Q861Y2 pygathrix b
16	129.5	22.2	146	6 Q861Y1	Q861Y1 pygathrix a

17	129	22.1	152	11 Q9JKI5	Q9JKI5 mus saxicol
18	127	21.8	157	11 Q9UKI9	Q9UKI9 meriones un
19	126.5	21.7	153	11 Q9UKI7	Q9UKI7 mus saxicol
20	126	21.6	157	11 Q9UKJ3	Q9UKJ3 meriones un
21	125.5	21.5	146	6 Q861Y4	Q861Y4 trachypithe
22	125	21.4	157	11 Q9UKJ4	Q9UKJ4 meriones un
23	123	21.1	154	11 Q9UKI8	Q9UKI8 mus saxicol
24	122	20.9	157	11 Q9UKJ1	Q9UKJ1 meriones un
25	121	20.8	147	6 Q7YRJ6	Q7YRJ6 balaena mys
26	121	20.7	157	11 Q9UKJ2	Q9UKJ2 meriones un
27	120.5	20.7	155	11 Q9UKH9	Q9UKH9 mus pahari
28	119.5	20.5	155	11 Q9UKI3	Q9UKI3 mus saxicol
29	118	20.2	147	6 Q7YRJ5	Q7YRJ5 tursiops tr
30	116.5	20.0	155	11 Q9UKI6	Q9UKI6 mus saxicol
31	115.5	19.8	132	6 Q9TV25	Q9TV25 eulemur ful
32	115.5	19.8	155	11 Q9UKI2	Q9UKI2 mus saxicol
33	115.5	19.8	155	11 Q9UKI4	Q9UKI4 mus saxicol
34	115	19.7	146	6 Q861Y5	Q861Y5 colobus gue
35	114.5	19.6	132	6 Q9TV24	Q9TV24 galago moho
36	114.5	19.6	170	6 Q9BEC1	Q9BEC1 tragulus ja
37	113.5	19.5	119	6 Q9TSQ6	Q9TSQ6 cercopithec
38	113.5	19.5	119	6 Q9TV32	Q9TV32 gorilla gor
39	113.5	19.5	147	6 Q8HZQ0	Q8HZQ0 pan troglod
40	113.5	19.5	155	11 Q9RL34	Q9RL34 rattus norv
41	113	19.4	156	11 Q9UKG6	Q9UKG6 mus caroli
42	113	19.4	156	11 Q9UKH7	Q9UKH7 mus caroli
43	112.5	19.3	119	6 Q9TV30	Q9TV30 saquinus oe
44	112.5	19.3	155	11 Q9RL25	Q9RL25 mus musculu
45	112.5	19.3	155	11 Q9UKH8	Q9UKH8 mus pahari

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76955.1; -;
DR PIR; A39035; A39035.
DR HSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 23 POTENTIAL.
127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.1%; Score 578; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 4e-59;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLTNRDVCNNINSTNLFHCKDKNTFYSPPEPKAICKGIASKNVLTT 61

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Q9JKJ3
ID Q9JKJ3 PRELIMINARY; PRT; 157 AA.
AC Q9JKJ3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 25.
GN EAR25.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238390; AAF67690.1; -.
DR HSSP; P10153; 1HI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNasePc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17945 MW; FDFE22FE77FE371A CRC64;

Query Match 21.1%; Score 122; DB 11; Length 157;
Best Local Similarity 29.2%; Pred. No. 3.4e-06;
Matches 33; Conservative 19; Mismatches 33; Indels 28; Gaps 6;

QY 3 WLTFQKKHLNTRDVCN-NILSTNLF--HCKDKNTFYSRPEPVKAICKGIIASKNVLT 59
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
36 WFTIQ--HISNTTTCQNAALGVNNYTCRCXDLNLFHLTRFANVNEC-----YNRNT 87
QY 60 TFE-----FYLSDCNVTS-----RPCKYKLLKSTNTFCVTCENQAP 95
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
88 TCKGRNCHDSRSVITDCNLTSPSTNYRCRYQRTARKFYRIACNNKTP 140

RESULT 15
Q9JKI9
ID Q9JKI9 PRELIMINARY; PRT; 157 AA.
AC Q9JKI9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Eosinophil-associated ribonuclease 44.
GN EAR44.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238394; AAF67694.1; -.
DR HSSP; P10153; 1HI2.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
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DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNasePc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17857 MW; 34FE2AE777FE3709 CRC64;

Query Match 21.1%; Score 122; DB 11; Length 157;
Best Local Similarity 29.4%; Pred. No. 3.4e-06;
Matches 32; Conservative 21; Mismatches 36; Indels 20; Gaps 7;

QY 3 WLTFQKKHLNTRDVCN-NILSTNLF--HCKDKNTFYSRPEPV-----KAICKGII 52
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
36 WFTIQ--HISNTTTCQNAALGVNNYTCRCXDLNLFHLTRFANVNECYNNTTCKY-- 91
QY 53 ASKNVL-TTFEYLSDCNVTS-----RPCKYKLLKSTNTFCVTCENQAP 95
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
92 GRNCHDSRSVITDCNLTSPSTNYRCRYQRTARKFYRIACNNKTP 140

Search completed: May 7, 2004, 21:46:01
Job time : 29.5753 secs
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Db      24  QNWETFOKKHLTTRDVYKCDAMKKKALFDCKQNTFYARPGRVQALCKNIIVSNVLST 83
QY      61  FEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGVGHC 104
Db      84  DEFYLSDCNRIKLPCHYKLLKKSNTICITCENKLPVHFVAVBEC 127

RESULT 5
Q9DFY7  PRELIMINARY; PRT; 128 AA.
AC      Q9DFY7;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RC-RNase3 ribonuclease precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
[1]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=20512555; PubMed=11058105;
RA      Liao Y.D., Huang H.C., Ieu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT      "Purification and cloning of cytotoxic ribonucleases from Rana
RT      catesbeiana (bullfrog).";
RL      Nucleic Acids Res. 28:4097-4104(2000).
DR      EMBL; AF242554; AAC31440.2; -.
DR      HSP; P22069; IONC.
DR      GO; GO:0003676; F:nucleic acid binding; IEA.
DR      GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR      InterPro; IPR001427; RNaseA.
DR      Pfam; PF000074; rnaseA; 1.
DR      ProDom; PD000535; RNaseA; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Signal.
FT      SIGNAL
FT      CHAIN
FT      SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 52.7%; Score 305; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 1.8e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0

QY      1  QDWLTFQKKHLNTRDVCNNILSNLPHCKDKKNTFYISREPPYKATCGIILASKNVLTT 60
Db      24  QDWETFOKKHLTTRDVYKCDVEMAKALFDCKTNTFYALPGRVKALCKNIIRDNDVLSR 83
QY      61  FEFYLSDCNVTSPCKYKLLKKSNTFCVTCENQAPVHFVGVGHC 104
Db      84  DAFLPQCDRIKLPCHYKLLKKSNTICITCVNQLPIHPAGVGSC 127

RESULT 6
Q9DFY5  PRELIMINARY; PRT; 128 AA.
AC      Q9DFY5;
DT      01-MAR-2001 (TrEMBLrel. 16, Created)
DT      01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      RC-RNase6 ribonuclease precursor.
OS      Rana catesbeiana (Bull frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
[1]
RN      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=20512555; PubMed=11058105;
RA      Liao Y.D., Huang H.C., Ieu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT      "Purification and cloning of cytotoxic ribonucleases from Rana
RT      catesbeiana (bullfrog).";

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Db 24 QDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 FEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953P90D351CFEE3 CRC64;

Query Match 94.5%; Score 547; DB 13; Length 127;
Best Local Similarity 94.2%; Pred. NO. 1.7e-55;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db 24 QDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 FEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

Query Match 65.6%; Score 380; DB 13; Length 128;
Best Local Similarity 66.3%; Pred. NO. 3.7e-36;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
DR PDB; 1KVZ; 28-JUL-02.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A62882B10ABDA CRC64;

Query Match 68.3%; Score 395.5; DB 13; Length 129;
Best Local Similarity 65.7%; Pred. NO. 5.9e-38;
Matches 69; Conservative 17; Mismatches 18; Indels 1; Gaps 1;

QY 1 QDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
Db 24 QDWLTFQKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 83
QY 61 FEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 128

RESULT 4
Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

Query Match 65.6%; Score 380; DB 13; Length 128;
Best Local Similarity 66.3%; Pred. NO. 3.7e-36;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 29.5753 Seconds
(without alignments)
1109,503 Million cell updates/sec

Title: US-09-961-400-4
Perfect score: 579
Sequence: 1 QWLTFOKKHLTNRDVCN.....TFCVTENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	569	98.3	127	13	Q918V8
2	547	94.5	127	13	Q8UVX5
3	395.5	68.3	129	13	Q9DFV6
4	380	65.6	128	13	Q9DFY8
5	305	52.7	128	13	Q9DFY7
6	303	52.3	128	13	Q9DFY5
7	292	50.4	133	13	Q98SM0
8	280	48.4	133	13	Q98SL9
9	279	48.2	132	13	Q98SM2
10	276	47.7	133	13	Q98SL8
11	274	47.3	132	13	Q98SM1
12	269.5	46.5	132	13	Q9DFV7
13	153.5	26.5	169	13	Q9W738
14	122	21.1	157	11	Q9UKJ3
15	122	21.1	157	11	Q9UKI9
16	120.5	20.8	146	6	Q861Y3

17	120.5	20.8	146	6	Q861Y2
18	120.5	20.8	146	6	Q861Y1
19	120	20.7	152	11	Q9UKI5
20	120	20.7	157	11	Q9UKJ4
21	117.5	20.3	153	11	Q9UKI7
22	117	20.2	157	11	Q9UKJ1
23	117	20.2	157	11	Q9UKJ2
24	116.5	20.1	146	6	Q861Y4
25	114.5	19.8	132	6	Q9TV24
26	114	19.7	147	6	Q7VRJ5
27	114	19.7	154	11	Q9UKI8
28	112	19.3	147	6	Q7VRJ6
29	111.5	19.3	155	11	Q9UKH9
30	110.5	19.1	119	6	Q9TSQ6
31	110.5	19.1	119	6	Q9TV32
32	110.5	19.1	132	6	Q9TV25
33	110.5	19.1	147	6	Q8HZQ0
34	110.5	19.1	155	11	Q9UKI3
35	109.5	18.9	119	6	Q9TV30
36	109	18.8	146	6	Q861Y5
37	108.5	18.7	155	11	Q9UKH8
38	108	18.7	156	11	Q923L6
39	107.5	18.6	155	11	Q9UKI6
40	107	18.5	124	6	Q95NE6
41	106.5	18.4	155	11	Q9UKI2
42	106.5	18.4	155	11	Q9RI34
43	106.5	18.4	155	11	Q9UKI4
44	105.5	18.2	144	11	Q80Z85
45	105.5	18.2	153	11	Q80XS4

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.
ID Q918V8
AC Q918V8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Onconase variant rapLR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAP76935.1; -
DR PIR; A39035; A39035.
DR HSP; P22069; IONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL
SQ SEQUENCE 1 23 POTENTIAL.
1 14491 MW; B8511DC5407AB69B CRC64;
127 AA;
Query Match 98.3%; Score 569; DB 13; Length 127;
Best local similarity 98.1%; Pred. No. 4.7e-58;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFOKKHLTNRDVCNIISTNLFHCKDKNTFYSPFVKAICKGLIASKNVLT 60

Search completed: May 7, 2004, 21:51:57
Job time : 35.2947 secs

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; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match          99.0%; Score 596; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 4.9e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 67

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 68 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 13
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match          99.0%; Score 596; DB 10; Length 117;
Best Local Similarity 98.2%; Pred. No. 4.9e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 67

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

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Db 68 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 14
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RacOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match          98.0%; Score 590; DB 10; Length 110;
Best Local Similarity 97.3%; Pred. No. 2.2e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNL 60

Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT

```

QY 61 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
|||
DB 61 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
|||

RESULT 9
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

Query March	99.0%	Score 596;	DB 10;	Length 111;
Best Local Similarity	99.1%	Prod. No. 4.6e-60;		
Matches 109;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps 0;				
QY	1	QNWATFOQKHINTPIICNTIMDNNIYIVGGQCKRVMTFIISATTVKAICTGVINNVL	60	
DB	2	QNWATFOQKHINTPIICNTIMDNNIYIVGGQCKRVMTFIISATTVKAICTGVINNVL	61	
QY	61	STTFPQNTCTRTSITPCCPSYSRSTETNYICVKCENYYPVHFAGIGRCP	110	
DB	62	STTFPQNTCTRTSITPCCPSYSRSTETNYICVKCENYYPVHFAGIGRCP	111	

RESULT 10
US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21

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;
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met (-1) RaCOR1 Met22Leu Met57Leu)
US-09-948-391A-21

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	Query Match	99.0%;	Score 596;	DB 10;	Length 111;
	Best Local Similarity	98.2%;	Pred No. 4.6e-60;		
	Matches 108;	Conservative 2;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QNWATQOQKHINTPICNTIMDNIIYVGGQCKRVNTFISSATTVKALCTGVINNVNL	60		
Db	2	QNWATQOQKHINTPICNTILDNIIYVGGQCKRVNTFISSATTVKALCTGVINNVNL	61		
Qy	61	STTRFQNLCTRTSIIPRCPYSSRTETNYICVKCENQYVPHFAGIRCP	110		
Db	62	STTRFQNLCTRTSIIPRCPYSSRTETNYICVKCENQYVPHFAGIRCP	111		

RESULT 11
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-21

Query Match	99.0%	Score 596	DB 10	Length 111
Best Local Similarity	98.2%	Pred. No. 4.6e-60		
Matches 108	Conservative	2	Mismatches 0	Indels 0
Gaps 0				
Qy	1	QNWATFOQKHIIINTPIICNTITMDNNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL	60	
Db	2	QNWATFOQKHIIINTPIICNTITMDNNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL	61	
Qy	61	STTTFQMLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP	110	
Db	62	STTTFQMLNCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP	111	

RESULT 12
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services

; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match
Best Local Similarity 99.2%; Score 597; DB 10; Length 110;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 6

US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-34311005
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) Rac0R1 Q1S)
US-09-948-391A-26

Query Match
Best Local Similarity 99.2%; Score 597; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 3 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 7

US-09-961-400-26

; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match
Best Local Similarity 99.2%; Score 597; DB 10; Length 111;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
DB 3 NWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 8

US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match
Best Local Similarity 99.0%; Score 596; DB 10; Length 110;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 60
DB 1 QNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 60

Db 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

RESULT 2

US-09-961-400-15

; Sequence 15, Application US/09961400

; Publication No. US20030124131A1

; GENERAL INFORMATION:

; APPLICANT: RYBAK, SUSANNA M.

; APPLICANT: GOLDENBERG, DAVID M.

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 018733/1059

; CURRENT APPLICATION NUMBER: US/09/961,400

; CURRENT FILING DATE: 2001-09-25

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/079,751

; PRIOR FILING DATE: 1998-03-26

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 15

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Rana catesbeiana

US-09-961-400-15

Query Match 100.0%; Score 602; DB 10; Length 110;

Best Local Similarity 100.0%; Pred. No. 9.5e-61;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
|||||

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

RESULT 3

US-09-961-400-17

; Sequence 17, Application US/09961400

; Publication No. US20030124131A1

; GENERAL INFORMATION:

; APPLICANT: RYBAK, SUSANNA M.

; APPLICANT: GOLDENBERG, DAVID M.

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 018733/1059

; CURRENT APPLICATION NUMBER: US/09/961,400

; CURRENT FILING DATE: 2001-09-25

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/079,751

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Rana catesbeiana

US-09-961-400-17

Query Match 100.0%; Score 602; DB 10; Length 110;

Best Local Similarity 100.0%; Pred. No. 9.5e-61;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
|||||

Db 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
|||||

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Query Match 100.0%; Score 602; DB 10; Length 111;

Best Local Similarity 100.0%; Pred. No. 9.6e-61;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 60
|||||

Db 2 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
|||||

QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111
|||||

RESULT 4

US-09-948-391A-24

; Sequence 24, Application US/09948391A

; Publication No. US20030027311A1

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: The United States of America

; APPLICANT: as represented by the Secretary of the

; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Recombinant Anti-tumor RNase

; FILE REFERENCE: 015280-343110US

; CURRENT APPLICATION NUMBER: US/09/948,391A

; CURRENT FILING DATE: 2002-05-10

; PRIOR APPLICATION NUMBER: US 60/079,751

; PRIOR FILING DATE: 1998-03-27

; PRIOR APPLICATION NUMBER: WO PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: US 09/622,613

; PRIOR FILING DATE: 2000-08-17

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 24

; LENGTH: 110

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:Rana

; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution

; OTHER INFORMATION: (recombinant RaCOR1 Q1S)

US-09-948-391A-24

Query Match 99.2%; Score 597; DB 10; Length 110;

Best Local Similarity 100.0%; Pred. No. 3.5e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 2 NWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINNNVL 61
|||||

QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
|||||

RESULT 5

US-09-961-400-24

; Sequence 24, Application US/09961400

; Publication No. US20030124131A1

; GENERAL INFORMATION:

; APPLICANT: RYBAK, SUSANNA M.

; APPLICANT: GOLDENBERG, DAVID M.

; APPLICANT: NEWTON, DIANNE L.

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT

; TITLE OF INVENTION: CELLS

; FILE REFERENCE: 018733/1059

; CURRENT APPLICATION NUMBER: US/09/961,400

; CURRENT FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: 09/622,613

; PRIOR FILING DATE: 2000-08-17

; PRIOR APPLICATION NUMBER: PCT/US99/06641

; PRIOR FILING DATE: 1999-03-26

; PRIOR APPLICATION NUMBER: 60/079,751

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 17

; LENGTH: 111

; TYPE: PRT

; ORGANISM: Rana catesbeiana

US-09-961-400-17

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.2947 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-15
Perfect score: 602
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKENQVPHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues
Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				* Query Match		Description	
Result No.	Score	Length	ID	DB	ID		
1	602	100.0	110	10	US-09-948-391A-15	Sequence 15, Appl	
2	602	100.0	110	10	US-09-961-400-15	Sequence 15, Appl	
3	602	100.0	111	10	US-09-961-400-17	Sequence 17, Appl	
4	597	99.2	110	10	US-09-948-391A-24	Sequence 24, Appl	
5	597	99.2	110	10	US-09-948-391A-26	Sequence 26, Appl	
6	597	99.2	111	10	US-09-948-391A-22	Sequence 22, Appl	
7	597	99.2	111	10	US-09-948-391A-22	Sequence 22, Appl	
8	596	99.0	110	10	US-09-961-400-19	Sequence 19, Appl	
9	596	99.0	111	10	US-09-948-391A-17	Sequence 17, Appl	
10	596	99.0	111	10	US-09-948-391A-21	Sequence 21, Appl	
11	596	99.0	111	10	US-09-961-400-21	Sequence 21, Appl	
12	596	99.0	117	10	US-09-948-391A-22	Sequence 22, Appl	
13	596	99.0	117	10	US-09-961-400-22	Sequence 22, Appl	
14	590	98.0	110	10	US-09-948-391A-19	Sequence 19, Appl	
15	281.5	46.8	104	10	US-09-961-400-2	Sequence 2, Appl	

16	281.5	46.8	105	10	US-09-948-391A-6	Sequence 6, Appl
17	281.5	46.8	105	10	US-09-961-400-6	Sequence 6, Appl
18	281.5	46.8	127	10	US-09-948-391A-28	Sequence 28, Appl
19	281.5	46.8	127	10	US-09-961-400-28	Sequence 28, Appl
20	280.5	46.6	104	10	US-09-948-391A-2	Sequence 2, Appl
21	278.5	46.3	111	10	US-09-961-400-9	Sequence 9, Appl
22	277.5	46.1	105	14	US-10-153-882-2	Sequence 11, Appl
23	276.5	45.9	104	10	US-09-948-391A-11	Sequence 11, Appl
24	276.5	45.9	104	10	US-09-961-400-11	Sequence 11, Appl
25	276.5	45.9	105	10	US-09-948-391A-13	Sequence 13, Appl
26	276.5	45.9	105	10	US-09-961-400-13	Sequence 13, Appl
27	275.5	45.8	104	10	US-09-948-391A-4	Sequence 4, Appl
28	275.5	45.8	104	10	US-09-961-400-4	Sequence 4, Appl
29	275.5	45.8	105	10	US-09-961-400-8	Sequence 8, Appl
30	272.5	45.3	104	9	US-09-986-119-1	Sequence 1, Appl
31	272.5	45.3	104	10	US-09-918-887-1	Sequence 1, Appl
32	269.5	44.8	104	12	US-10-461-713-53	Sequence 53, Appl
33	266.5	44.3	105	10	US-09-948-391A-8	Sequence 8, Appl
34	266.5	44.3	111	10	US-09-948-391A-9	Sequence 9, Appl
35	206	34.2	83	9	US-09-986-119-3	Sequence 3, Appl
36	206	34.2	83	10	US-09-918-887-3	Sequence 3, Appl
37	163	27.1	169	13	US-10-016-447-2	Sequence 2, Appl
38	135.5	22.5	124	12	US-10-037-417-103	Sequence 103, App
39	131.5	21.8	119	12	US-10-016-248-89	Sequence 89, Appl
40	131.5	21.8	119	15	US-10-074-978A-139	Sequence 139, App
41	121	20.1	99	15	US-10-074-978A-141	Sequence 141, App
42	117.5	19.5	124	12	US-10-461-713-52	Sequence 52, Appl
43	117	19.4	147	9	US-09-731-872-254	Sequence 254, App
44	117	19.4	147	10	US-09-876-997-254	Sequence 254, App
45	114.5	19.0	124	9	US-09-981-286A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match 100.0%; Score 602; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.5e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNWATFOQKHINTPIICNTMDNNIYVGQCKRYNTFTLISSATTVKATCTGVNNVYL 60
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; ORGANISM: Rana pipiens
US-09-961-400-9
Query Match      46.6%; Score 279.5; DB 10; Length 111;
Best Local Similarity 49.5%; Pred. No. 7.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYIVGGQCKRVNTFTIISATTVKALCTGVI-NLN 58
   |::|||::||:|::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 8 QDWLTFQKKHLTNRDVCNNILSTNLF---HCKDKNTFIYSRPEPVKALCKGLIASKN 63
   |::|||::||:|::|||::|||::|||::|||::|||::|||::|||::|||::|||:

Qy 59 VLSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
   |::|||::||:|::|||::|||::|||::|||::|||::|||::|||::|||::|||:
Db 64 VLTITSEFYLSDC---NVTISRECKYKLKSTNTFCVTCENQAPVHFVGVGHC 111
   |::|||::||:|::|||::|||::|||::|||::|||::|||::|||::|||::|||:
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Search completed: May 7, 2004, 21:51:58
Job time : 35.2947 secs

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; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCORI Q1S)
US-09-948-391A-26

Query Match          98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 61
DB 3 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 62
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 13
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

Query Match          98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 61
DB 3 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 62
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCORI Q1S)
US-09-948-391A-26

Query Match          98.5%; Score 591; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 61
DB 3 NWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 62
QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 13
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-26

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DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 14
US-09-948-391A-17
; Sequence 17, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RaCOR1)
US-09-948-391A-17

Query Match          98.3%; Score 590; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 5e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QNWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 60
DB 2 QNWATFOQKHINTPIICNTIIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNVLS 61
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT

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; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 100.0%; Score 600; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 67
Qy 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 68 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 6
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RacOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match 99.3%; Score 596; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Qy 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Query Match 99.3%; Score 596; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Qy 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match 99.3%; Score 596; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Qy 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 8
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match 99.3%; Score 596; DB 10; Length 111;
Best Local Similarity 98.2%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Qy 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Sat May 8 17:57:17 2004

US-09-961-400-21

Query Match 100.0%; Score 600; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.7e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 2 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 61
QY 61 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111

RESULT 4

US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met (-1) RACOR1 Met22Leu Met57Leu-(His)6)

US-09-948-391A-22

Query Match 100.0%; Score 600; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.9e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 8 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 67
QY 61 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 68 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 117

RESULT 5

US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400

RESULT 2

US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met (-1) RACOR1 Met22Leu Met57Leu)

US-09-948-391A-21

Query Match 100.0%; Score 600; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.7e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
Db 2 QNWATFQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 61
QY 61 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRCPYSSRTETNYICVKENQYPVHFAGIGRCP 111

RESULT 3

US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.2947 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 277566755 residues

Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	110	10	US-09-961-400-19
2	600	100.0	111	10	US-09-948-391A-21
3	600	100.0	111	10	US-09-961-400-21
4	600	100.0	117	10	US-03-948-391A-22
5	600	100.0	117	10	US-09-961-400-22
6	596	99.3	110	10	US-09-948-391A-15
7	596	99.3	110	10	US-09-961-400-15
8	596	99.3	111	10	US-09-961-400-17
9	594	99.0	110	10	US-09-948-391A-19
10	591	98.5	110	10	US-03-948-391A-24
11	591	98.5	110	10	US-09-961-400-24
12	591	98.5	111	10	US-09-948-391A-26
13	591	98.5	111	10	US-09-961-400-26
14	590	98.3	111	10	US-09-948-391A-17
15	279.5	46.6	111	10	US-09-961-400-9

16	277.5	46.2	104	10	US-09-961-400-2	Sequence 2, Appli
17	277.5	46.2	105	10	US-09-948-391A-6	Sequence 6, Appli
18	277.5	46.2	105	10	US-09-961-400-6	Sequence 6, Appli
19	277.5	46.2	127	10	US-09-948-391A-28	Sequence 28, Appli
20	277.5	46.2	127	10	US-09-961-400-28	Sequence 2, Appli
21	276.5	46.1	104	10	US-09-948-391A-2	Sequence 4, Appli
22	276.5	46.1	104	10	US-09-948-391A-4	Sequence 8, Appli
23	276.5	46.1	104	10	US-09-961-400-4	Sequence 2, Appli
24	276.5	46.1	105	10	US-09-961-400-8	Sequence 4, Appli
25	273.5	45.6	105	14	US-10-153-882-2	Sequence 8, Appli
26	272.5	45.4	104	10	US-09-948-391A-11	Sequence 2, Appli
27	272.5	45.4	104	10	US-09-961-400-11	Sequence 11, Appli
28	272.5	45.4	105	10	US-09-948-391A-13	Sequence 11, Appli
29	272.5	45.4	105	10	US-09-961-400-13	Sequence 13, Appli
30	268.5	44.8	104	9	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.8	104	10	US-09-918-887-1	Sequence 1, Appli
32	267.5	44.6	105	10	US-09-948-391A-8	Sequence 8, Appli
33	267.5	44.6	111	10	US-09-948-391A-9	Sequence 9, Appli
34	265.5	44.2	104	12	US-10-461-713-53	Sequence 53, Appli
35	202	33.7	83	9	US-09-986-119-3	Sequence 3, Appli
36	202	33.7	83	10	US-09-918-887-3	Sequence 3, Appli
37	161	26.8	169	13	US-10-016-447-2	Sequence 2, Appli
38	131.5	21.9	124	12	US-10-037-417-103	Sequence 103, App
39	127.5	21.2	119	12	US-10-016-248-89	Sequence 89, Appli
40	127.5	21.2	119	15	US-10-074-378A-139	Sequence 139, App
41	118	19.7	99	15	US-10-074-378A-141	Sequence 141, App
42	117	19.5	147	9	US-09-731-872-254	Sequence 254, App
43	117	19.5	147	10	US-09-876-997-254	Sequence 254, App
44	114	19.0	123	12	US-10-461-713-58	Sequence 58, Appli
45	114	19.0	124	13	US-10-016-447-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match 100.0%; Score 600; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.7e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNWATFOQKHINTPIICNTLDNNIYVGGCKVNTFISSATTVKATGVINLVL 60
Db 1 QNWATFOQKHINTPIICNTLDNNIYVGGCKVNTFISSATTVKATGVINLVL 60
QY 61 STTRFQLNCTRTSTTPPCYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQLNCTRTSTTPPCYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Search completed: May 7, 2004, 21:46:03
Job time : 31.2816 secs

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QBCECI          PRELIMINARY;      PRT;       170 AA.
IID Q9BEC1
AAC Q80285;
AC   Q80285;    PRELIMINARY;      PRT;       144 AA.
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DST  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DDT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Brain-type ribonuclease ribonuclease precursor (Fragment).
GN   RNASE B.
OS   Tragus javanicus (Lesser Malay chevrotain).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OTC  Tragulidae; Tragulus.
OX   NCBI_TaxID=9849;
[!]_TaxID=9849;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21347458; PubMed=11453981;
RA   Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RR   Warmels H.W., Beintema J.J.;
RT   "Secretory ribonucleases in the primitive ruminant chevrotain
RTE  (Tragus javanicus)".
RT   (Tragus javanicus)".
RL   Eur. J. Biochem. 268:3890-3897(2001).
RC   -/- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC   EMBL; AJ271299; CAC24723.1; -.
DR   HSSP; P00656; ILSQ.
DR   GO; GO:0004519; F:endonuclease activity; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR   InterPro; IPR001427; RNaseA.
DR   Pfam; PF00074; rnaseA; 1.
DR   PRINTS; PR00794; RIBONUCLEASE.
DR   ProDom; PD000535; RNaseA; 1.
DR   SMART; SM00092; RNase Pc; 1.
DR   PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW   Endonuclease; Hydrolase; Nuclease; Signal.
FT   NON_TER     1
FT   SIGNAL      <1
FT   CHAIN       20
SQ   SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;
Query Match              21.8%; Score 131; DB 6; Length 170;
Best Local Similarity    33.1%; Pred. No. 2.8e-07;
Matches                   4; Conservative               17; Mismatches 46; Indels 20; Gaps 7;

Qy   4 ATPOKHI-----INTPIONTMNNIYIVGCKRVNFISSATTWKAICT----- 52
    |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   25 AKFRQHLDAGNSSINSN-YCNLMWKRR-KMTGRCKPVNTFIESUEDVKAICSEKNIT 82
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy   53 ---GVINNMVLSTRFPOLNTCTRTSITPRP-CPYSSSRTRTNVICVKEN--QYPVFHAGI 106
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db   83 CKNGOPNC HQSNST-MNI TDCROTGGSKVPNCAYKTSQKKYII VACEGTFSVPVHFDS 141
    |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Qy           107 GRCP 110
DB            142 AVL P 145

RESULT 15
Q80Z85          PRELIMINARY;      PRT;       144 AA.
ID Q80Z85
AC Q80Z85;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DST  01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DDT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Angiogenin-4.
GN   ANG4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OTC  NCBI_TaxID=10090;
OX   [1]
RN   [1]
RP   SEQUENCE FROM N.A.
RX   STRAIN=NMR1;
RC   MEDLINE=22493143; PubMed=12548285;
RX   MEDLINE=22493143; PubMed=12548285;
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RESULT 11		Q9DFY7	
ID	Q9DFY7	PRELIMINARY;	PRT; 128 AA.
AC	Q9DFY7;		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-OCT-2001	(TrEMBLrel. 18, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	RC-RNase3 ribonuclease precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.		
OX	NCBI_TaxID=8400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEDLINE=20512555; PubMed=11058105;		
RA	Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.-C.;		
RT	"Purification and cloning of cytotoxic ribonucleases from Rana		
RT	catesbeiana (bullfrog).";		
RL	Nucleic Acids Res. 28:4097-4104(2000).		
DR	EMBL; AF242554; AAG31440.2; -		
DR	HSSP; P22069; 10NC.		
DR	GO; GO:0003676; F:nucleic acid binding; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnaseA; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KW	Signal.		
FT	SIGNAL.	1 23	POTENTIAL.
FT	CHAIN	24 128	RC-RNASE3 RIBONUCLEASE.
SQ	SEQUENCE	128 AA; 14517 MW; 2B14986082E0587D CRC64;	
Query Match 37.6%; Score 226.5; DB 13; Length 128;			
Best Local Similarity 41.1%; Pred. NO. 1.5e-18;			
Matches 46; Conservative 18; Mismatches 39; Indels 9; Gaps 4;			
Qy	1	QNWATFQOKHINT-PIICNTIMDNNIYVGQCKRVNTPIISATTVKALCTGV-INMN 58	
Db	24	QDWETFFQKHLTDYKVKCDVEMAKALF---DCKNTTFIYALPGRVKALCKNRDNTD 79	
Qy	59	VLSTTRFOLNCTRTSITPRPCPYSSRTNYIVCKENQYVHPAGIGRCP 110	
Db	80	VLSRDAFLLPQCDRIKL--PCHYKLSSNTTICITCNQLPIHFAGVGSCTP 128	
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ID	Q9DFY5		
AC	Q9DFY5;		
DT	01-MAR-2001	(TrEMBLrel. 16, Created)	
DT	01-OCT-2001	(TrEMBLrel. 18, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	RC-RNase6 ribonuclease precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.		
OX	NCBI_TaxID=8400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEDLINE=20512555; PubMed=11058105;		
RA	Liao Y.D., Huang H.C., Leu Y.-J., Wei C.W., Tang P.C., Wang S.-C.;		
RT	"Purification and cloning of cytotoxic ribonucleases from Rana		
RT	catesbeiana (bullfrog).";		
RL	Nucleic Acids Res. 28:4097-4104(2000).		
DR	HSSP; P22069; 10NC.		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RC	MEDLINE=20512555; PubMed=11058105;		
RA	Liao Y.D., Huang H.C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;		
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF242556; AAG31442.2; -		
DR	HSSP; P22069; 10NC.		

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RESULT 8
Q8UVX5 PRELIMINARY; PRT; 127 AA.
ID Q8UVX5 AC Q8UVX5
DT 01-MAR-2002 (TREMELrel. 20, Created)
DT 01-MAR-2002 (TREMELrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RQ Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR PIR; A39035; A39035.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
KW SIGNAL.
FT SIGNAL
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 46.1%; Score 277.5; DB 13; Length 127;
Best Local Similarity 49.5%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 24 QWLTFQKHINTRDVDCNIMSNLFP-----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 59 VLSTTRFQNLCTRTSITRPPCPYSRSTRTNYICVKCENQYPVHFAGIGRCP 109
Db 80 VLTTFSEFYLSDC---NVTSRCKPKYKLSKSNKFCVTCENQAPVHFVGVGSC 127

RESULT 9
Q9DFY6 PRELIMINARY; PRT; 129 AA.
ID Q9DFY6 AC Q9DFY6
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-OCT-2001 (TREMELrel. 18, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RQ TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 24 QWLTFQKHINTRDVDCNIMSNLFP-----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 59 VLSTTRFQNLCTRTSITRPPCPYSRSTRTNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLTTFSEFYLSDCNRKIL---PCHYKLSKSNITCITCNKLPVHFVAVEECP 128

Query Match 38.1%; Score 229.5; DB 13; Length 128;
Best Local Similarity 40.2%; Pred. No. 6.7e-19;
Matches 45; Conservative 20; Mismatches 38; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 24 QWLTFQKHINTRDVDCNIMSNLFP-----HCKDKNTFIYSRPEPVKAICKGIASKN 79

QY 59 VLSTTRFQNLCTRTSITRPPCPYSRSTRTNYICVKCENQYPVHFAGIGRCP 110
Db 80 VLTTFSEFYLSDCNRKIL---PCHYKLSKSNITCITCNKLPVHFVAVEECP 128

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RESULT 5
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match
Best Local Similarity 74.5%; Score 448.5; DB 13; Length 132;
Matches 86; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 59
Db 23 QDWPTFOQKHIPSTSSIDCNTIMDKIYVIRGQCKVNTFIYSATTVKAICTGVINSV 82

QY 60 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 83 LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 127

RESULT 6
Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289642; AAG30414.2; -.

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DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;

Query Match
Best Local Similarity 62.5%; Score 376; DB 13; Length 132;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 22 QWAKFKKHITSTSSIDCNTIMDKAIYVGGCKERTFTIISSEDNVKAICGVSPPDRK 81

QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 82 ELSTTSFKLNTCIRDSITPRCPYHPSDNNKICVCKEQLPVHFVGIGKC 132

RESULT 7
Q918V8 ID Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Onconase variant rapIR1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure.";
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR PIR; A39035; A39035.
DR HSSP; P22069; 1ONC.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match
Best Local Similarity 46.8%; Score 281.5; DB 13; Length 127;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
Db 24 QDWLTFQKHINTTRDVCNIMSNLF----HCKDKNTFIYSRPFVKAICGIIASKN 79

QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 80 VLITSEFYLSDC---NVTSRCKYKLKSTNTFCVTCENQAPVHFVGIGHC 127

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Sat May 8 17:57:15 2004

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RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 79.5%; Score 478.5; DB 13; Length 133;
Best Local Similarity 78.4%; Pred. No. 6.2e-48;
Matches 87; Conservative 11; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFQOKHIINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 59
DB 23 QNWATFQOKHIINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 59
QY 60 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
DB 83 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 133

RESULT 4
Q98SL8 PRELIMINARY; PRT; 133 AA.
ID Q98SL8
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSSP; P11916; 1BC4.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;

Query Match 78.3%; Score 471.5; DB 13; Length 133;
Best Local Similarity 76.6%; Pred. No. 4.1e-47;
Matches 85; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFQOKHIINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 59
DB 23 QNWATFQOKHIINTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 59
QY 60 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
DB 83 LSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRCP 133

us-09-961-400-15.rspt
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:10 ; Search time 31.2816 Seconds
(without alignments)
1109.503 Million cell updates/sec

Title: US-09-961-400-15

Perfect score: 602

Sequence: 1 QNWATFQCKHIINTPIICNT.....ICVKCENQVPHFAGTGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mbc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvivirus:*
 - 16: sp_bacterioph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560.5	93.1	133	13	Q98SM0 rana catesb
2	487.5	81.0	132	13	Q98SM2 rana catesb
3	478.5	79.5	133	13	Q98SL9 rana catesb
4	471.5	78.3	133	13	Q98SL8 rana catesb
5	448.5	74.5	132	13	Q98SM1 rana catesb
6	376	62.5	132	13	Q9DF78 rana catesb
7	281.5	46.8	127	13	Q918V8 rana catesb
8	277.5	46.1	127	13	Q8UVX5 rana pipien
9	246	40.9	129	13	Q9DFY6 rana catesb
10	229.5	38.1	128	13	Q9DFY8 rana catesb
11	226.5	37.6	128	13	Q9DFY7 rana catesb
12	217.5	36.1	128	13	Q9DFY5 rana catesb
13	163	27.1	169	13	Q9W738 xenopus lae
14	131	21.8	170	6	Q9BEC1
15	128.5	21.3	144	11	Q90Z85
16	128.5	21.3	153	11	Q90X84

17	127.5	21.2	147	6	Q7YR76	Q7YR76 balaena mys
18	126	20.9	150	11	Q8VD94	Q8VD94 berylmys bo
19	125.5	20.8	163	6	Q9BDC2	Q9BDC2 antilocapra
20	124.5	20.7	116	6	Q9TVC0	Q9TVC0 sus scrofa
21	124	20.6	150	11	Q8VD88	Q8VD88 rattus norv
22	122.5	20.3	144	6	Q9BH14	Q9BH14 antilocapra
23	121.5	20.2	147	6	Q7YR75	Q7YR75 tursiops tr
24	121	20.1	146	6	Q861Y5	Q861Y5 colobus gue
25	120.5	20.0	149	11	Q8K2T2	Q8K2T2 mus musculu
26	120.5	20.0	149	11	Q8C6G3	Q8C6G3 mus musculu
27	120	19.9	150	11	Q8VD92	Q8VD92 rattus exul
28	119.5	19.9	146	6	Q861Y4	Q861Y4 trachypithe
29	118.5	19.7	146	6	Q861Y3	Q861Y3 pygathrix r
30	118.5	19.7	146	6	Q861Y2	Q861Y2 pygathrix b
31	118.5	19.7	146	6	Q861Y1	Q861Y1 pygathrix a
32	116.5	19.4	152	11	Q8VD89	Q8VD89 rattus norv
33	114.5	19.0	124	6	Q9SNE6	Q9SNE6 bubalus bub
34	112.5	18.7	148	11	Q8C7E4	Q8C7E4 mus musculu
35	112.5	18.7	149	11	Q8VD95	Q8VD95 berylmys bo
36	112	18.6	134	6	Q9BDB9	Q9BDB9 tragulus ja
37	111.5	18.5	152	11	Q8VD84	Q8VD84 rattus tior
38	111.5	18.5	156	6	Q8SQ05	Q8SQ05 lagothrix l
39	111	18.4	148	11	Q8C6E3	Q8C6E3 mus musculu
40	110.5	18.4	119	6	Q9TV28	Q9TV28 eulemur ful
41	110.5	18.4	119	6	Q9TV30	Q9TV30 saguinus oe
42	109.5	18.2	142	6	Q9BEC3	Q9BEC3 tragulus ja
43	109.5	18.2	156	6	Q8SQ06	Q8SQ06 atales geof
44	109	18.1	124	6	Q9BEC2	Q9BEC2 tragulus ja
45	108.5	18.0	156	6	Q8SQ08	Q8SQ08 saimiri sci

ALIGNMENTS

RESULT 1

Q98SM0	PRELIMINARY;	PRT;	133 AA.
ID	Q98SM0		
AC	Q98SM0;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	RNase A-type ribonuclease rc208 precursor.		
OS	Rana catesbeiana (Bull frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.		
OX	NCBI_TaxID=9400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21539506; PubMed=11683320;		
RA	Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;		
RT	"Rapid diversification of RNase A superfamily ribonuclease from the		
RT	bullfrog, Rana catesbeiana."		
RL	J. Mol. Evol. 53:31-38(2001).		
DR	EMBL; AF351209; AAK30255.1; -.		
DR	HSSP; P11916; 1BC4.		
DR	GO; CO:0003676; F:nucleic acid binding; IEA.		
DR	GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnaseA; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_PC; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KW	Signal.		
FT	SIGNAL		
SQ	SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;		

Query Match 93.1%; Score 560.5; DB 13; Length 133;
Best Local Similarity 94.6%; Pred. No. 1.7e-57;
Matches 105; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
QY 1 QNWATFQCKHIINTPII-CNTIMDNNIYVGQCKRVNTFIISATTVAICTGVIMNV 59
DB 23 QNWATFQCKHIINTPII-CNTIMDNNIYVGQCKRVNTFIISATTVAICTGVIMNV 82


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/
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/875,811
/ FILING DATE: 19-FEB-1998
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/02588
/ FILING DATE: 19-FEB-1997
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 358 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-875-811-51

Query Match 45.8%; Score 277.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 4.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFOOKHIINT-PIICNTIMDNNTYIVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFYSPPEPVKAICKGIIASK 56
Qy 59 NVLTSTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTSTSEYVLSDC---NVTSPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 105

RESULT 14
US-08-875-811-26
; Sequence 26, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998

/
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/875,811
/ FILING DATE: 19-FEB-1997
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: WO PCT/US97/02588
/ FILING DATE: 19-FEB-1997
/ INFORMATION FOR SEQ ID NO: 26:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 105 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-875-811-26

Query Match 45.6%; Score 276.5; DB 3; Length 105;
Best Local Similarity 49.1%; Pred. No. 1.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFOOKHIINT-PIICNTIMDNNTYIVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MSDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFYSPPEPVKAICKGIIASK 56
Qy 59 NVLTSTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTSTSEYVLSDC---NVTSPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 105

RESULT 15
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,971
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,180
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
/ LENGTH: 105 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-875-811-26

Query Match 45.6%; Score 276.5; DB 3; Length 105;
Best Local Similarity 49.1%; Pred. No. 1.2e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFOOKHIINT-PIICNTIMDNNTYIVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MSDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFYSPPEPVKAICKGIIASK 56
Qy 59 NVLTSTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTSTSEYVLSDC---NVTSPCKYKLLKSTNKFVCVTCENQAPVHFVGVGSC 105
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Qy 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
 Db 262 MSDWLTQKKHITNTRDVCNDIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 317
 Qy 59 NVLSTTRFQNTCTRTSITPRPCYSRTEINVCVCENQYPVHFAGIGRC 110
 Db 318 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVTCENQAPVHFVGVGSC 366

RESULT 11

US-08-875-811-39
 ; Sequence 39, Application US/08875811
 ; Patent No. 6045793
 ; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: Boque, Lluís
 ; APPLICANT: Wlodawer, Alexander
 ; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/875,811
 ; FILING DATE: 19-FEB-1998
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US97/02588
 ; FILING DATE: 19-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/011,800
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Faris, Susan K.

REGISTRATION NUMBER: 41,739
 ; REFERENCE/DOCKET NUMBER: 015280-244100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 105 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-875-811-39

Query Match 45.8%; Score 277.5; DB 3; Length 105;
 Best Local Similarity 49.1%; Pred. No. 9.4e-25;
 Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
 Db 1 MEDWLTQKKHITNTRDVCNDIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56
 Qy 59 NVLSTTRFQNTCTRTSITPRPCYSRTEINVCVCENQYPVHFAGIGRC 110
 Db 57 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 12

US-08-875-811-41

; Sequence 41, Application US/08875811
 ; Patent No. 6045793
 ; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: Boque, Lluís
 ; APPLICANT: Wlodawer, Alexander
 ; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA

ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/875,811
 ; FILING DATE: 19-FEB-1998
 ; CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: WO PCT/US97/02588
 ; FILING DATE: 19-FEB-1997
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/011,800
 ; FILING DATE: 21-FEB-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Faris, Susan K.

REGISTRATION NUMBER: 41,739
 ; REFERENCE/DOCKET NUMBER: 015280-244100US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 355 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-875-811-41

Query Match 45.8%; Score 277.5; DB 3; Length 355;
 Best Local Similarity 49.1%; Pred. No. 4.1e-24;
 Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
 Db 251 MEDWLTQKKHITNTRDVCNDIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 306
 Qy 59 NVLSTTRFQNTCTRTSITPRPCYSRTEINVCVCENQYPVHFAGIGRC 110
 Db 307 NVLTSEFYLSDC---NVTSRPKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 13

US-08-875-811-51
 ; Sequence 51, Application US/08875811
 ; Patent No. 6045793
 ; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: Boque, Lluís
 ; APPLICANT: Wlodawer, Alexander
 ; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor

```
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-57

Query Match          46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 1 MSDWLTFOKKHITNTDRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASK 56

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
DB 57 NVLTTSFYLSDC---NVTSRCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note= "E6FB[Met-(-1)]SerrOnc"
; US-08-875-811-64

Query Match          46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
DB 251 MSDWLTFOKKHITNTDRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASK 306

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQVPHFAGIGRC 110
DB 307 NVLTTSFYLSDC---NVTSRCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 10
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-55

Query Match          46.5%; Score 281.5; DB 3; Length 366;
Best Local Similarity 50.0%; Pred. No. 1.5e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
```

```

; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

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Query Match 46.5%; Score 281.5; DB 3; Length 254;
Best Local Similarity 50.0%; Pred. No. 9.5e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MSDWLTFFQKHINTTRDVCDCNIMSTNLP---HCKDKNTFIYSRPEPVKAICKGIASK 56
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 NVLSTTRFQNLCTRTSITPRPCPSYSRRTETNYICVKCENQYVPHFAGIGRC 110
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 NVLTTSFYLSDC---NVTSRPCKYKLRKSTNFKVCVCENQAPVPHFVGVCSC 105
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```

```

RESULT 7
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

```

```

Query Match 46.5%; Score 281.5; DB 3; Length 355;
Best Local Similarity 50.0%; Pred. No. 1.4e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 251 MSDWLTFFQKHINTTRDVCDCNIMSTNLP---HCKDKNTFIYSRPEPVKAICKGIASK 306
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 59 NVLSTTRFQNLCTRTSITPRPCPSYSRRTETNYICVKCENQYVPHFAGIGRC 110
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 307 NVLTTSFYLSDC---NVTSRPCKYKLRKSTNFKVCVCENQAPVPHFVGVCSC 355
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 8
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800

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DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 46.6%; Score 282.5; DB 1; Length 104;
Best Local Similarity 50.0%; Pred. No. 2.4e-25;
Matches 55; Conservative 15; Mismatches 31; Indels 9; Gaps 4;

QY 3 MSNATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVAICTGVI-NMV 60
Db 2 DNLTFQKHVNTTRDVCNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASKV 57
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 58 LTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 104

RESULT 4
US-08-875-811-32
; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-32

Query Match 46.5%; Score 281.5; DB 3; Length 112;
Best Local Similarity 50.0%; Pred. No. 3.5e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVAICTGVI-NM 58
Db 8 MSDLTFQKHVNTTRDVCNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASK 63
QY 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110

Db 64 NVLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 112

RESULT 5
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-59

Query Match 46.5%; Score 281.5; DB 3; Length 251;
Best Local Similarity 50.0%; Pred. No. 9.3e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 MSNATFOQKHINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVAICTGVI-NM 58
Db 147 MSDLTFQKHVNTTRDVCNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIASK 202
QY 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 203 NVLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 251

RESULT 6
US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

```
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-891-848-12

Query Match          96.8%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 NWATFOQKHIIPTII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNVL 61
Db 2 NWATFOQKHIIPTIINCNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNVL 61

QY 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111
Db 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
```

```
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-875-811-8

Query Match          96.8%; Score 586.5; DB 3; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 3 NWATFOQKHIIPTII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNVL 61
Db 2 NWATFOQKHIIPTIINCNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNVNVL 61

QY 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111
Db 62 STTRFQINTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.5747 Seconds
(without alignments)
345.738 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNWATFOQHIIPTIICN.....ICVKCENQPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*
- 2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
- 3: /cgn2_6/ptodata/2/iaa/5A-COMB.pep:*
- 4: /cgn2_6/ptodata/2/iaa/5B-COMB.pep:*
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- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586.5	96.8	111	2	US-08-891-848-12
2	586.5	96.8	111	3	US-08-875-811-8
3	282.5	46.6	104	1	US-08-467-955-2
4	281.5	46.5	112	3	US-08-875-811-32
5	281.5	46.5	251	3	US-08-875-811-59
6	281.5	46.5	254	3	US-08-875-811-61
7	281.5	46.5	355	3	US-08-875-811-49
8	281.5	46.5	355	3	US-08-875-811-57
9	281.5	46.5	355	3	US-08-875-811-64
10	281.5	46.5	366	3	US-08-875-811-55
11	277.5	45.8	105	3	US-08-875-811-39
12	277.5	45.8	355	3	US-08-875-811-41
13	277.5	45.8	358	3	US-08-875-811-51
14	276.5	45.6	105	3	US-08-875-811-26
15	272.5	45.0	104	1	US-08-283-971-1
16	272.5	45.0	104	1	US-07-921-619-1
17	272.5	45.0	104	1	US-08-467-955-1
18	272.5	45.0	104	2	US-08-891-848-13
19	272.5	45.0	104	3	US-08-875-811-1
20	272.5	45.0	104	3	US-09-394-268-1
21	272.5	45.0	104	4	US-09-071-672-1
22	272.5	45.0	104	4	US-09-687-748-1
23	272.5	45.0	104	4	US-08-626-288-1
24	272.5	45.0	104	4	US-09-095-429-1
25	272.5	45.0	104	4	US-09-986-119-1
26	272.5	45.0	106	3	US-08-875-811-28
27	272.5	45.0	107	3	US-08-875-811-30

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RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

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ALIGNMENTS

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28 272.5 45.0 129 3 US-08-875-811-63
29 272.5 45.0 358 3 US-08-875-811-45
30 272.5 45.0 365 3 US-08-875-811-53
31 272.5 45.0 379 3 US-08-875-811-43
32 270.5 44.6 105 3 US-08-875-811-24
33 269.5 44.5 104 4 US-08-626-288-2
34 269.5 44.5 104 4 US-09-095-429-2
35 267.5 44.1 104 3 US-09-394-268-2
36 267.5 44.1 104 4 US-09-687-748-2
37 254.5 42.0 107 3 US-08-875-811-20
38 239.5 39.5 111 3 US-08-875-811-22
39 236.5 39.0 360 3 US-08-875-811-47
40 235 38.8 114 3 US-09-223-118-3
41 226 37.3 114 3 US-09-223-118-2
42 225 37.1 114 3 US-09-223-118-1
43 224 37.0 114 3 US-09-223-118-4
44 206 34.0 83 3 US-08-875-811-2
45 206 34.0 83 4 US-09-071-672-3

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Sequence 63, Appl
Sequence 45, Appl
Sequence 53, Appl
Sequence 43, Appl
Sequence 24, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 47, Appl
Sequence 3, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
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Sequence 3, Appl

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Job time : 13.5611 secs

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QY 59 NVL-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104
Db 62 NVACKNGQNCYQSYSTMSITDCRETGSSKYPNCAKTKQAKHIIIVACEGNPYVPVHY 120
RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megalera rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastria, W.; Wellings, G.W.; Beintema, J.J.
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent
Query Match 20.1%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.7e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;
QY 7 FQOKHI-----INTPIICNTIMNNIYIVGGCKRVNTFISSATVKAIC----- 52
Db 7 FQGHMDTEHSTASSNYCNLMKAR-DMTSGRCKPLNTHPEKSVDAVCHQENVTCK 65
QY 53 TGVNNVLTTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104
Db 66 NGRNLC-YKSNRLSITNCRQTSKYPNCOYETSNLKQIIVACEGQYVPVHF 118
RESULT 12
NRUC
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A06512; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 19.9%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.5e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;
QY 7 FQOKHI-----INTPIICNTIMNNIYIVGGCKRVNTFISSATVKAICGVINMV 60
Db 8 FERQHMDSRGSPSTNYCNEMKSR-NMTQGRCKPVNTFVHESLADVQAVC---FQKNV 63
QY 61 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104
Db 64 LCKNGQNCYQSNMHIITDCRTSNDYCNCSYRSQEKSIIVACEGNPYVPVHF 120

RESULT 13
NRMS
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:G200762; PIDN:AAA40060.1; PID:G200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:G53981; PIDN:CAA42697.1; PID:G53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 19.9%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.5e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;
QY 7 FQOKHI-----INTPIICNTIMNNIYIVGGCKRVNTFISSATVKAICGVINMV 60
Db 33 FQGHMDPDGSSINSPTYCNQMKRR-DMTNGSKPVNTFVHESLADVQAVCS---QENV 88
QY 61 L-----STTRFQLNCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 104
Db 89 TCKNRKSNCKYSSSALHITDCHLKGNSKYPNCDYKTKTQYQKHIIIVACEGNPYVPVHF 145
RESULT 14
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BN>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease
Query Match 19.7%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.7e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

S20066
pancreatic-type ribonuclease (EC 3.1.27.5) Brb precursor, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C:Accession: S20066; JX0056
R:Sasano, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri, N.; Nucleic Acids Res. 19, 6469-6474, 1991
A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A:Reference number: S20066; MUID:92093604; PMID:1754384
A:Accession: S20066
A:Molecule type: DNA
A:Residues: 1-167 <SAS>
A:Cross-references: EMBL:X59767; NID:gl50; PIDN:CAA42439.1; PID:gl51
R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A:Title: Primary structure of a ribonuclease from bovine brain.
A:Reference number: JX0056; MUID:89214015; PMID:3243767
A:Accession: JX0056
A:Molecule type: protein
A:Residues: 27-154, 'S', 156-166 <WAT>
A:Experimental source: brain
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase
F:38,67,145/Active site: His, Lys, His #status predicted
F:52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 22.0%; Score 133.5; DB 2; Length 167;
Best Local Similarity 31.4%; Pred. No. 3.7e-06;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 5 ATFOQKHI-----INTPLICNTIMDNNIYVGQCKRVNTFIISATTVKAICTGVINM 58
DB 32 AKFRQHMDSGSSSSSNFYCNQMRR-RWTHGRCKPVNTFVHESLDVKAICS---QK 87
QY 59 NVL-----STTRFQNLCTRTSITPRP-CPYSSRTETNYICVCKE-NOY-PVHFA 105
DB 88 NITKNGHPNCVQSTWSITDCRTGSGKYENCAYKTSQKQYITVACEGPPYVPHFD 147
QY 106 G 106
DB 148 G 148

RESULT 8
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pig
N:Alternate names: RNase A
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A92071; A91391; A00816
R:Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A:Reference number: A92071; MUID:70104197; PMID:5460946
A:Accession: A92071
A:Molecule type: protein
A:Residues: 1, 'Q', 3-124 <JAC>
R:Wierenga, R.K.; Huijzga, J.D.; Gaastra, W.; Welling, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A:Reference number: A91391
A:Accession: A91391
A:Molecule type: protein
A:Residues: 1-124 <WIE>
R:Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A:Reference number: A92072; MUID:70104198; PMID:4904878
A:Contents: annotation; disulfide bonds
C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.9%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 3.4e-06;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FQCKHI-----INTPLICNTIMDNNIYVGQCKRVNTFIISATTVKAICTGV-INNM 59
DB 8 FORHMDPSSSSSNFYCNQMRR-NMTQGRCKPVNTFVHESLDVKAICSQINNVCK 66
QY 60 VLSTTRFQNLCTRTSITPRP-CPYSSRTETNYICVCKENQ--YPVHF 104
DB 67 NGQTCYQSNTHMTDCRTGSGKYENCAYKTSQKQYITVACEGPPYVPHF 120

RESULT 9
S4111
pancreatic ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S4111; MUID:94139745; PMID:9307028
A:Accession: S4111
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match 20.9%; Score 126.5; DB 2; Length 119;
Best Local Similarity 29.8%; Pred. No. 1.3e-05;
Matches 34; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 3 NWATFQKHI-----INTPLICNTIMDNNIYVGQCKRVNTFIISATTVKAICT--- 52
DB 2 DWSSFQNKHIDYPTFSASPNAYCDLMMQRR-NLAPTKCKTNTFVHAPSEIQVCGSG 60
QY 53 -TGVINMNVLTTRFQNLCTRTSIT-PRPCPYSSRTETNYICVCKENQYPVHF 104
DB 61 GTHVEDNLYDSNESFDLTDCKNVGTFAPSSCKYNGTPGKTRIRIACENQPVHF 114

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Antilocapra americana (pronghorn)
C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gaastra, W.; Munniksma, J.
J. Mol. Evol. 13, 305-316, 1979
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw
A:Reference number: A00813; MUID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BEI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.2%; Score 122.5; DB 1; Length 124;
Best Local Similarity 30.3%; Pred. No. 3.4e-05;
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY 5 ATFOQKHIINTPI-----ICNTIMDNNIYVGQCKRVNTFIISATTVKAICTGVINM 58
DB 119 G 119

RESULT 7

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:31:13 ; Search time 13.5611 Seconds
(without alignments)
787.345 Million cell updates/sec

Title: US-09-961-400-26
Perfect score: 606
Sequence: 1 MSNWATFQKHIIPTIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	586.5	96.8	111	2 A27121	ribonuclease-relat
2	450	74.3	111	1 JX0120	ribonuclease-relat
3	369	60.9	111	2 JX0085	pancreatic ribonuc
4	272.5	45.0	104	2 A39035	ribonuclease-relat
5	135.5	22.4	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.4	145	1 A35932	angiogenin precurs
7	133.5	22.0	167	2 S20066	pancreat-type ri
8	132.5	21.9	124	1 NRP6	pancreatic ribonuc
9	126.5	20.9	119	2 S41111	pancreatic ribonuc
10	122.5	20.2	124	1 NRP6	pancreatic ribonuc
11	122	20.1	122	1 NRP6	pancreatic ribonuc
12	120.5	19.9	128	1 NRCU	pancreatic ribonuc
13	120.5	19.9	149	1 NRCU	pancreatic ribonuc
14	119.5	19.7	123	1 A43825	angiogenin - pig
15	118.5	19.6	128	1 NRCU	pancreatic ribonuc
16	117.5	19.4	128	1 NRCU	pancreatic ribonuc
17	116.5	19.2	124	1 NRCU	pancreatic ribonuc
18	116.5	19.2	124	1 NRCU	pancreatic ribonuc
19	116.5	19.2	124	1 NRCU	pancreatic ribonuc
20	116.5	19.2	128	1 NRCU	pancreatic ribonuc
21	114.5	18.9	124	2 S08549	ribonuclease - dom
22	114	18.8	125	1 A32474	angiogenin [valida
23	113.5	18.7	125	1 NRDEO	pancreatic ribonuc
24	113.5	18.7	125	1 B43825	angiogenin - rabbi
25	113	18.6	147	1 NRHUG	angiogenin precurs
26	112.5	18.6	124	1 NRCU	pancreatic ribonuc
27	112.5	18.6	124	1 NRDEO	pancreatic ribonuc
28	111.5	18.4	130	2 S22808	pancreatic ribonuc
29	110.5	18.2	124	1 NRBO	pancreatic ribonuc

30	110.5	18.2	124	1 NRWB	pancreatic ribonuc
31	110.5	18.2	124	1 NREKN	pancreatic ribonuc
32	110.5	18.2	124	2 S07141	pancreatic ribonuc
33	110.5	18.2	150	1 NRBO	pancreatic ribonuc
34	110.5	18.2	158	2 I61900	eosinophil-derived
35	109.5	18.1	124	1 NRSH	pancreatic ribonuc
36	108.5	17.9	119	2 JX0115	pancreatic ribonuc
37	108.5	17.9	124	1 NRBO	pancreatic ribonuc
38	108.5	17.9	152	1 NRRP	pancreatic ribonuc
39	106.5	17.6	124	1 NRRP	pancreatic ribonuc
40	106.5	17.6	125	4 A47498	seminal ribonuclea
41	106.5	17.6	150	1 NRBO	seminal ribonuclea
42	104.5	17.2	124	1 NRGN	pancreatic ribonuc
43	104.5	17.2	124	1 NRDEP	pancreatic ribonuc
44	104	17.2	125	2 S04503	pancreatic ribonuc
45	103.5	17.1	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C:Accession: A27121
R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi
Biochemistry 26, 2189-2194, 1987
A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A:Reference number: A27121; MUID:87299649; PMID:3304421
A:Accession: A27121
A:Molecule type: protein
A:Residues: 1-111 <TIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin

Query Match 96.8%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.5e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy	3	NWATFQKHIIPTII-CNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINMNVL 61
Db	2	NWATFQKHIIPTIINCNTIMDNNIYVGGQCKRVNTFIISATVKAICTGVINMNVL 61
Qy	62	STTRFQNTCTRTSTTPPCPSSTRTNYICVKCENQYPVHFAGIGRCP 111
Db	62	STTRFQNTCTRTSTTPPCPSSTRTNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi
J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JX0120; MUID:91035319; PMID:2229005
A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyrrolidone carboxylic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.3%; Score 450; DB 1; Length 111;
Best Local Similarity 78.2%; Pred. No. 9e-38; Mismatches 7; Indels 2; Gaps 2;


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OS Rana pipiens.
OS Synthetic.
XX WO9731116-A2.
XX 28-AUG-1997.
XX 19-FEB-1997; 97WO-US002588.
XX 21-FEB-1996; 96US-0011800P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX N-PSDB; AAT94972.
XX Ribonuclease molecules based on native Oncinase - used for killing cells,
XX particularly tumour cells.
XX Disclosure; Page 76; 90pp; English.
XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX (rOnc) which are modifications of the RNase Oncinase (RTM) (nOnc). Such
XX novel ribonuclease molecules are highly cytotoxic and can be used alone
XX or to form chemical conjugates or to target recombinant immunofusions.
XX They are used particularly for decreasing tumour cell growth. They can
XX also be used for cell separation in vitro by selectively killing unwanted
XX types of cells, e.g. in bone marrow prior to transplantation into a
XX patient undergoing marrow ablation by radiation, or for killing leukaemia
XX cells or T-cells that would cause graft versus host disease. The toxins
XX can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnc and also
XX lower immunogenicity in humans
XX Sequence 251 AA;
XX
XX Query Match 46.5%; Score 281.5; DB 2; Length 251;
XX Best Local Similarity 50.0%; Pred. NO. 8.7e-24;
XX Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
XX
QY 1 MSNWATFOOKHIINT-PIICNTIMDNINIVGQCKRVNTFISSATTVAICTGVI-NM 58
DB 147 MSDWLTFOKKHITNTRDVCDDNIMSTNLF----HCKDKNTFIYSRPEPVAICKGLIASK 202
XX
QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 203 NVLTTFSEFVLSDC---NVTSRPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 251
XX
RESULT 13
AAW35135
ID AAW35135 standard; protein; 254 AA.
XX
AC AAW35135;
XX
XX 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 11.
XX
XX RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX
XX Rana pipiens.
XX Synthetic.
XX WO9731116-A2.
XX 28-AUG-1997.
XX 19-FEB-1997; 97WO-US002588.
XX 21-FEB-1996; 96US-0011800P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX N-PSDB; AAT94972.
XX Ribonuclease molecules based on native Oncinase - used for killing cells,
XX particularly tumour cells.
XX Disclosure; Page 77; 90pp; English.
XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX (rOnc) which are modifications of the RNase Oncinase (RTM) (nOnc). Such
XX novel ribonuclease molecules are highly cytotoxic and can be used alone
XX or to form chemical conjugates or to target recombinant immunofusions.
XX They are used particularly for decreasing tumour cell growth. They can
XX also be used for cell separation in vitro by selectively killing unwanted
XX types of cells, e.g. in bone marrow prior to transplantation into a
XX patient undergoing marrow ablation by radiation, or for killing leukaemia
XX cells or T-cells that would cause graft versus host disease. The toxins
XX can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnc and also
XX lower immunogenicity in humans
XX Sequence 254 AA;
XX
XX Query Match 46.5%; Score 281.5; DB 2; Length 254;
XX Best Local Similarity 50.0%; Pred. NO. 8.8e-24;
XX Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
XX
QY 1 MSNWATFOOKHIINT-PIICNTIMDNINIVGQCKRVNTFISSATTVAICTGVI-NM 58
DB 1 MSDWLTFOKKHITNTRDVCDDNIMSTNLF----HCKDKNTFIYSRPEPVAICKGLIASK 56
XX
QY 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
DB 57 NVLTTFSEFVLSDC---NVTSRPCKYKLLKSTNKFCVTCENQAPVHFVGVGSC 105
XX
RESULT 14
AAW35133
ID AAW35133 standard; protein; 355 AA.
XX
AC AAW35133;
XX
XX 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase rOnc fusion protein 9.
XX
XX RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX tumour cell growth; frog.
XX
XX Rana pipiens.
XX Synthetic.
XX WO9731116-A2.
XX 28-AUG-1997.
XX 19-FEB-1997; 97WO-US002588.
XX 21-FEB-1996; 96US-0011800P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Rybak SM, Newton DL, Boque L, Wlodawer A;
XX WPI; 1997-435168/40.
XX N-PSDB; AAT94971.
XX

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RESULT 10
AAW28867.
ID AAY28867 standard; protein; 105 AA.
XX AC AAY28867;
XX DT 25-JAN-2000 (first entry)
XX DE Recombinant Met(-1) RaPLR1.
XX KW Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
XX KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
XX KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XX KW autoimmune disease.
XX OS Rana pipiens.
XX OS Synthetic.
XX FT Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
XX PN WO9950398-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US006641.
XX PR 27-MAR-1998; 98US-0079751P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL;
XX DR WPI; 1999-610847/52.
XX DR N-PSDB; AAZ08126.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases.
XX PS Claim 34; Page 57; 71pp; English.
XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
XX CC protein with Met at position 1. Carboxy terminal end of recombinant
XX CC RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
XX CC antibody directed against CD22 on cancerous B cells or human chorionic
XX CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
XX CC ribonucleases can be expressed in bacteria without an N-terminal
XX CC methionine due to the presence of a signal peptide that is cleaved by
XX CC bacteria. The soluble expression of ribonuclease allows the proteins to
XX CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX CC proteins. They can be used for treatment of cancer and autoimmune
XX CC diseases
XX SQ Sequence 105 AA;
Query Match 46.5%; Score 281.5; DB 2; Length 105;
Best Local Similarity 49.1%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
Qy 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NM 58
Db 1 MQDWLTFQKKHLATNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56
Qy 59 NVLSTTRFQNLTCRTISITPRPCYSRSTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTTSEFYLSDC---NVTSRPCYKYLKSTNFCVTCENQAPVHFVGVGHC 105
RESULT 11
AAW35118
ID AAW35118 standard; protein; 112 AA.
XX AC AAW35118;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase protein NLSMetSerrOnc.
XX KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX KW tumour cell growth; frog.
XX OS Rana pipiens.
XX PN WO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97WO-US002588.
XX PR 21-FEB-1996; 96US-0011800P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Boque L, Wlodawer A;
XX DR WPI; 1997-435168/40.
XX DR N-PSDB; AAT94955.
XX PT Ribonuclease molecules based on native Onconase - used for killing cells,
XX PT particularly tumour cells.
XX PS Claim 18; Page 63; 90pp; English.
XX CC AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are
XX CC modifications of the RNase Onconase (rNm) (nOnc). Such novel ribonuclease
XX CC molecules are highly cytotoxic and can be used alone or to form chemical
XX CC conjugates or to target recombinant immunofusions. They are used
XX CC particularly for decreasing tumour cell growth. They can also be used for
XX CC cell separation in vitro by selectively killing unwanted types of cells,
XX CC e.g. in bone marrow prior to transplantation into a patient undergoing
XX CC marrow ablation by radiation, or for killing leukaemia cells or T-cells
XX CC that would cause graft versus host disease. The toxins can also be used
XX CC to selectively kill unwanted cells in culture. The new ribonucleases have
XX CC increased cytotoxic activity compared to nOnc and also lower
XX CC immunogenicity in humans
XX SQ Sequence 112 AA;
Query Match 46.5%; Score 281.5; DB 2; Length 112;
Best Local Similarity 50.0%; Pred. No. 3.2e-24;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
Qy 1 MSNWATFOQKHINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVAICTGVI-NM 58
Db 8 MSDWLTFQKKHLATNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63
Qy 59 NVLSTTRFQNLTCRTISITPRPCYSRSTETNYICVKCENQYVHFAGIGRC 110
Db 64 NVLTTSEFYLSDC---NVTSRPCYKYLKSTNFCVTCENQAPVHFVGVGSC 112
RESULT 12
AAW35134
ID AAW35134 standard; protein; 251 AA.
XX AC AAW35134;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 10.
XX KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
XX KW tumour cell growth; frog.

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aps 4;

• •

weight

2

fewer

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aps      4;
NMNV    60
: ||
SKNV    57
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Sequence 110 AA:

This invention describes a novel nucleic acid construct comprising sequences encoding functional pancreatic RNase and a second protein (preferably the light and heavy chains of an antibody) which binds a specific cell surface marker on a target cell and functions as a cytotoxic agent. The products can be used for selectively killing cells expressing a specific surface marker. They can be used for treating tumors or infected cells (e.g. cells infected by viruses (especially latent or chronic virus infections, such as human immunodeficiency virus (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, cytomegalovirus)) and cells infected with parasites (such as the malaria parasite). They can also be used for treating immune dysfunctional cells in immune and autoimmune diseases. Additionally, they may be used as contraceptives. Finally they can also be used for cell separation *in vitro* by selectively killing unwanted types of cells (e.g. in bone marrow) prior to transplantation into a patient undergoing marrow ablation by radiation or for killing leukemia cells or T-cells that would cause graft-versus-host disease. This sequence represents a full-length

CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX
 SQ Sequence 110 AA;

Query Match 99.2%; Score 601; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 7.9e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61
 DB 1 SNWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 60
 QY 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111
 DB 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 4
 AAY28872
 ID AAY28872 standard; protein; 110 AA.
 AC AAY28872;
 XX

25-JAN-2000 (first entry)

Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 RNase.

Rana catesbeiana.

Synthetic.

WO9950398-A2.

07-OCT-1999.

26-MAR-1999; 99WO-US006641.

27-MAR-1998; 98US-0079751P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Rybak SM, Newton DL;

WPI; 1999-610847/52.

N-PSDB; AA208130.

New recombinant ribonucleases, used for killing target cells, e.g. for
 treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 62; 71pp; English.

The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 protein encoded by a cDNA modified for expression in E. coli. Carboxy
 terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 which can be a LL2 antibody directed against CD22 on cancerous B cells or
 human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
 cells. Recombinant ribonucleases can be expressed in bacteria without an
 N-terminal methionine due to the presence of a signal peptide that is
 cleaved by bacteria. The soluble expression of ribonuclease allows the
 proteins to be fused in-frame with ligand binding moieties to form
 cytotoxic fusion proteins. They can be used for treatment of cancer and
 autoimmune diseases

Sequence 110 AA;

Query Match 98.5%; Score 597; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.3e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 NWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 62
 DB 2 NWATFOQKHIIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNVLS 61

QY 63 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111

DB 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 5

AAY28876

ID AAY28876 standard; protein; 111 AA.

AC AAY28876;

25-JAN-2000 (first entry)

Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.

Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
 recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 cancer; bullfrog; RNase; autoimmune disease.

Rana catesbeiana.

Synthetic.

Key Location/Qualifiers

FT Misc-difference 1

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 23

FT Misc-difference 23 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 58

FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

FT Misc-difference 58

FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

WO9950398-A2.

07-OCT-1999.

26-MAR-1999; 99WO-US006641.

27-MAR-1998; 98US-0079751P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Rybak SM, Newton DL;

WPI; 1999-610847/52.

N-PSDB; AA208133.

New recombinant ribonucleases, used for killing target cells, e.g. for
 treating cancers, viral infections or autoimmune diseases.

Claim 22; Page 66; 71pp; English.

The present sequence is a recombinant Rana catesbeiana oocyte
 ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 has a covalently bound ligand binding moiety, which can be a LL2 antibody
 directed against CD22 on cancerous B cells or human chorionic
 gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 ribonucleases can be expressed in bacteria without an N-terminal
 methionine due to the presence of a signal peptide that is cleaved by
 bacteria. The soluble expression of ribonuclease allows the proteins to
 be fused in-frame with ligand binding moieties to form cytotoxic fusion
 proteins. They can be used for treatment of cancer and autoimmune
 diseases

CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX Sequence 111 AA;

Query Match 100.0%; Score 606; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.1e-61;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSNWATFQQKHINTPIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MSNWATFQQKHINTPIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2
 AAY28873
 ID AAY28873 standard; protein; 111 AA.

AC AAY28873;
 DT 25-JAN-2000 (first entry)
 DE Recombinant Met (-1) RaCOR1.
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT
 XX WO9950398-A2.
 PD 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL;
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08131.
 XX
 FT New recombinant ribonucleases, used for killing target cells, e.g. for
 FT treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 63; 71pp; English.

CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an

CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX Sequence 111 AA;

Query Match 99.3%; Score 602; DB 2; Length 111;
 Best Local Similarity 99.1%; Pred. No. 6.1e-61;
 Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSNWATFQQKHINTPIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 DB 1 MQNWATFQQKHINTPIICNTIMDNNTIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
 QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
 DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3
 AAY28877
 ID AAY28877 standard; protein; 110 AA.

AC AAY28877;
 DT 25-JAN-2000 (first entry)
 DE Recombinant RaCOR1 GlnSer amino acid sequence.
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 GlnSer; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
 FT
 XX WO9950398-A2.
 PD 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL;
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08131.
 XX
 FT New recombinant ribonucleases, used for killing target cells, e.g. for
 FT treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 67; 71pp; English.

CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with GlnSer. Carboxy terminal end of
 CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:23:43 ; Search time 50.7285 Seconds
(without alignments)

618.248 Million cell updates/sec

Title: US-09-961-400-26

Perfect score: 606

Sequence: 1 MSNATFQKHINTPIICN.....ICVKCNQVPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	606	100.0	111	2	AAY28878 Recombina
2	602	99.3	111	2	AAY28873 Recombina
3	601	99.2	110	2	AAY28877 Recombina
4	597	98.5	110	2	AAY28872 Recombina
5	596	98.3	111	2	AAY28876 Recombina
6	591	97.5	110	2	AAY28874 Recombina
7	586.5	96.8	111	2	AAY33321 Frog lect
8	285.5	47.1	105	2	AAY28871 Recombina
9	282.5	46.6	104	2	AAY28877 Recombina
10	281.5	46.5	105	2	AAY28867 Recombina
11	281.5	46.5	112	2	AAY35118 R. pipien
12	281.5	46.5	251	2	AAY35134 R. pipien
13	281.5	46.5	254	2	AAY35135 R. pipien
14	281.5	46.5	355	2	AAY35133 R. pipien
15	281.5	46.5	355	2	AAY35129 R. pipien
16	281.5	46.5	366	2	AAY35132 R. pipien
17	280.5	46.3	104	2	AAY28870 Recombina
18	278.5	46.0	105	2	AAY28869 Recombina
19	277.5	45.8	105	2	AAY35123 R. pipien
20	277.5	45.8	105	2	AAY39400 Recombina
21	277.5	45.8	355	2	AAY35125 R. pipien
22	277.5	45.8	358	2	AAY35130 R. pipien
23	276.5	45.6	104	2	AAY28865 Rana pipi
24	276.5	45.6	105	2	AAY35116 R. pipien
25	276.5	45.6	127	2	AAY28879 Rana pipi

26	273.5	45.1	104	2	AAY28866	Aay28866 Recombina
27	272.5	45.0	104	2	AAR12344	Aar12344 Protein w
28	272.5	45.0	104	2	AAR47303	Aar47303 ONCONASE
29	272.5	45.0	104	2	AAW00736	AAW00736 Protein d
30	272.5	45.0	104	2	AAW14065	AAW14065 Onconase
31	272.5	45.0	104	2	AAW06543	AAW06543 Antitumou
32	272.5	45.0	104	2	AAW30301	AAW30301 Recombina
33	272.5	45.0	104	2	AAW88233	AAW88233 Rana pipi
34	272.5	45.0	104	2	AAY33322	Aay33322 Frog onco
35	272.5	45.0	104	4	AAW31666	AAW31666 Amino aci
36	272.5	45.0	104	5	ABG32650	ABG32650 Northern
37	272.5	45.0	106	2	AAW35122	AAW35122 R. pipien
38	272.5	45.0	107	2	AAW35117	AAW35117 R. pipien
39	272.5	45.0	358	2	AAW35127	AAW35127 R. pipien
40	272.5	45.0	365	2	AAW35131	AAW35131 R. pipien
41	272.5	45.0	379	2	AAW35126	AAW35126 R. pipien
42	270.5	44.6	105	2	AAW35115	AAW35115 R. pipien
43	269.5	44.5	104	2	AAW30302	AAW30302 Recombina
44	267.5	44.1	104	4	AAW31667	AAW31667 Amino aci
45	267.5	44.1	104	5	ABG31617	ABG31617 Northern

ALIGNMENTS

RESULT 1

AAY28878

ID AAY28878 standard; protein; 111 AA.

AC AAY28878;

DT 25-JAN-2000 (first entry)

DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.

XX Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1; covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; CD22; RNase; autoimmune disease.

XX Rana catesbeiana.

OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

FT WO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US006641.

PR 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rybak SM, Newton DL;

PI WPI; 1999-610847/52.

XX N-PSDB; AAZ08135.

XX New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.

PS Claim 22; Page 68; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana ribonuclease

CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end

CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which

Search completed: May 11, 2004, 14:37:53
Job time : 16.4253 secs

RESULT 13

US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match 45.3%; Score 272.5; DB 1; Length 104;
Best Local Similarity 49.1%; Pred. No. 3.5e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 2 NWATFOOKHINT-PIICNTIMNNIYVGGQCKRVNTFTIISATTVKAICTGVI-MNMV 59
DB 2 DMLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGLIASKNV 57
QY 60 LSTTRFQNLNCTSTITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 58 LTTSEFYLSDC---NVTSRCKYKLLKSKTNKFCVTENQAPVHFVGVGSC 104

RESULT 14

US-08-891-848-13
; Sequence 13, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..104
; OTHER INFORMATION: /label= Onc
; OTHER INFORMATION: /note= "Onconase from Rana pipiens"
US-08-891-848-13

Query Match 45.3%; Score 272.5; DB 2; Length 104;
Best Local Similarity 49.1%; Pred. No. 3.5e-24;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 2 NWATFOOKHINT-PIICNTIMNNIYVGGQCKRVNTFTIISATTVKAICTGVI-MNMV 59
DB 2 DMLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGLIASKNV 57
QY 60 LSTTRFQNLNCTSTITPRCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 58 LTTSEFYLSDC---NVTSRCKYKLLKSKTNKFCVTENQAPVHFVGVGSC 104

RESULT 15

58 LTTSEFYLSDC--NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

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; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-57

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 355;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58
Db 2 SOWLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 57

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 58 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
US-08-875-811-57

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 355;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58
Db 2 SOWLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 57

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 58 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 9
US-08-875-811-64
; Sequence 64, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; MOLECULE TYPE: protein
US-08-875-811-57

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 355;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58
Db 2 SOWLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 57

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 58 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 9
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-55

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 366;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..355
; OTHER INFORMATION: /note= "B6FB [Met-(-1)]SerrOnc"
US-08-875-811-64

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 355;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-NMN 58
Db 252 SOWLTFQKKHINTRDVDCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 307

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 308 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 10
US-08-875-811-55
; Sequence 55, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 366 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-55

Query Match
Best Local Similarity 46.0%; Score 276.5; DB 3; Length 366;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
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; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

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Query Match 46.0%; Score 276.5; DB 3; Length 254;
Best Local Similarity 49.5%; Pred. No. 3.6e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 2 SDMLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 58 VLTTSEFLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

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RESULT 7
US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

Query Match 46.0%; Score 276.5; DB 3; Length 355;
Best Local Similarity 49.5%; Pred. No. 5.4e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 58
Db 252 SDMLTFQKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 307

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 308 VLTTSEFLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

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RESULT 8
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800

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DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 47.0%; Score 282.5; DB 1; Length 104;

Best Local Similarity 50.0%; Pred. No. 2.4e-25; Mismatches 15; Gaps 4;

Matches 55; Conservative 15; Indels 9; Gaps 4;

QY 2 NWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-MNV 59

Db 2 DWLTFQKHVTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKV 57

QY 60 LETTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 58 LTTSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 4

US-08-875-811-32

; Sequence 32, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 32:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 112 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-875-811-32

Query Match 46.0%; Score 276.5; DB 3; Length 112;

Best Local Similarity 49.5%; Pred. No. 1.3e-24;

Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-MNV 58

Db 9 SDWLFQKHVTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKV 64

QY 59 VLSTTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 65 VLTTSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGSC 112

RESULT 5

US-08-875-811-59

; Sequence 59, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

; APPLICANT: Wlodawer, Alexander

; TITLE OF INVENTION: Recombinant Ribonuclease Proteins

; NUMBER OF SEQUENCES: 64

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/875,811

; FILING DATE: 19-FEB-1998

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US97/02588

; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/011,800

; FILING DATE: 21-FEB-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Paris, Susan K.

; REGISTRATION NUMBER: 41,739

; REFERENCE/DOCKET NUMBER: 015280-244100US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 576-0200

; TELEFAX: (415) 576-0300

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 251 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-875-811-59

Query Match 46.0%; Score 276.5; DB 3; Length 251;

Best Local Similarity 49.5%; Pred. No. 3.5e-24;

Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-MNV 58

Db 148 SDWLFQKHVTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKV 203

QY 59 VLSTTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109

Db 204 VLTTSEFYLSDC---NVTSPCKYKLKSTNKFVTCENQAPVHFVGVGSC 251

RESULT 6

US-08-875-811-61

; Sequence 61, Application US/08875811

; Patent No. 6045793

; GENERAL INFORMATION:

; APPLICANT: Rybak, Susanna M.

; APPLICANT: Newton, Dianne L.

; APPLICANT: Boque, Lluís

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
; US-08-891-848-12
Query Match 97.6%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 NWATFOQKHIIPTII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVNVL 60
Db 2 NWATFOQKHIIPTIINCNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVNVL 61
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111
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US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faxis, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
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; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
; US-08-875-811-8
Query Match 97.6%; Score 586.5; DB 3; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.9e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 2 NWATFOQKHIIPTII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVNVL 60
Db 2 NWATFOQKHIIPTIINCNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVINNVNVL 61
QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111
RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:33:03 ; Search time 16.4253 Seconds
(without alignments)
345.738 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFQKHIINTPIICNT.....ICVKCNQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:**
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:**
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:**
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:**
- 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:**
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	97.6	111	2	US-08-891-848-12
2	586.5	97.6	111	3	US-08-875-811-8
3	282.5	47.0	104	1	US-08-467-955-2
4	276.5	46.0	112	3	US-08-875-811-32
5	276.5	46.0	251	3	US-08-875-811-59
6	276.5	46.0	254	3	US-08-875-811-61
7	276.5	46.0	355	3	US-08-875-811-49
8	276.5	46.0	355	3	US-08-875-811-57
9	276.5	46.0	355	3	US-08-875-811-64
10	276.5	46.0	366	3	US-08-875-811-55
11	272.5	45.3	104	1	US-08-283-971-1
12	272.5	45.3	104	1	US-07-921-619-1
13	272.5	45.3	104	1	US-08-467-955-1
14	272.5	45.3	104	2	US-08-891-848-13
15	272.5	45.3	104	3	US-08-875-811-1
16	272.5	45.3	104	3	US-09-394-268-1
17	272.5	45.3	104	4	US-09-071-672-1
18	272.5	45.3	104	4	US-09-687-748-1
19	272.5	45.3	104	4	US-08-626-228-1
20	272.5	45.3	104	4	US-09-095-429-1
21	272.5	45.3	104	4	US-09-986-119-1
22	272.5	45.3	105	3	US-08-875-811-39
23	272.5	45.3	105	3	US-08-875-811-28
24	272.5	45.3	106	3	US-08-875-811-30
25	272.5	45.3	107	3	US-08-875-811-63
26	272.5	45.3	129	3	US-08-875-811-41
27	272.5	45.3	353	3	US-08-875-811-41
28	272.5	45.3	358	3	US-08-875-811-51

28	272.5	45.3	379	3	US-08-875-811-43	Sequence 43, Appl
29	271.5	45.2	105	3	US-08-875-811-26	Sequence 26, Appl
30	269.5	44.8	104	4	US-08-626-288-2	Sequence 2, Appl
31	269.5	44.8	104	4	US-09-095-429-2	Sequence 2, Appl
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33	267.5	44.5	104	4	US-09-687-748-2	Sequence 2, Appl
34	267.5	44.5	105	3	US-08-875-811-24	Sequence 24, Appl
35	267.5	44.5	358	3	US-08-875-811-45	Sequence 45, Appl
36	267.5	44.5	365	3	US-08-875-811-53	Sequence 53, Appl
37	253.5	42.2	107	3	US-08-875-811-20	Sequence 20, Appl
38	239.5	39.9	111	3	US-08-875-811-22	Sequence 22, Appl
39	235	39.1	114	3	US-09-223-118-3	Sequence 3, Appl
40	231.5	38.5	360	3	US-08-875-811-47	Sequence 47, Appl
41	226	37.6	114	3	US-09-223-118-2	Sequence 2, Appl
42	225	37.4	114	3	US-09-223-118-1	Sequence 1, Appl
43	224	37.3	114	3	US-09-223-118-4	Sequence 4, Appl
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45	206	34.3	83	4	US-09-071-672-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: NO. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

Search completed: May 11, 2004, 14:35:04
Job time : 9.95475 secs

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Qy 58 NVL-----SYTRFOLNCTRTSITPRP-CYSSSTETNYICVKENQ--YPVVHF 10
Db 62 NITCKNGQPNCYQSNSTWNITDRGSSKYNPCKYTSQKQKYYITACEGDPYVPVHF 120

RESULT 12
ANG2_BOVIN STANDARD; PRT; 123 AA.
ID ANG2_BOVIN STANDARD; PRT; 123 AA.
AC P80929;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-2 (EC 3.1.27.-).
GN ANG2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCHI_taxID=9913;
RN [1]
RP SEQUENCE.
RC TISSUE=Milk, and Serum;
RX MEDLINE=97409980; PubMed=9266695;
RA Strydom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RT primary structure of angiogenin-2";
RL Eur. J. Biochem. 247:535-544(1997).
CC -1- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -1- TISSUE SPECIFICITY: Serum and milk.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P10152; IAGI.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC..).
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 123;
Best Local Similarity 30.6%; Pred. No. 6.8e-07;
Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps

Qy 6 FQOKHIINTPI-----ICNTIMDNNIYVGGCKRVNTFTIISATTVKAIK---TGVINM 57
Db 8 FLRKHYPDPTGHDDRYCNFMERR--NMTRPKCTNTFTIHGNSDDIRAVCDNRNGEYR 65

RESULT 13
RNER_GIRCA STANDARD; PRT; 141 AA.
ID RNER_GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
Qy 58 NVLSTTR--FQLNCTRTSITPRP-PCPYSSRTETNYICVKSNQYPPVH 102
Db 66 NGLERSRSPFQVTTCHRRGSGRPSPCKRYAFRANRVIVIRCDRGFFIH 113


```


Matches	38;	Conservative	17;	Mismatches	43;	Indels	23;	Gaps	7;
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QY	4	ATFOQKH	-----INTPICTIMDNNIYIVGGQCKRVNTFISSATTYKAICTGVINM	57
		: : :	: : :	
Db	32	AKFRQHMDSGSSSSNPYCNQMKRR	-RMTHGRCCKPVNTFVHESLDDVKAVGS--QK	87
QY	58	NVL	-----STTRFQNLCTRTSI	PRP
		: :	: :	
Db	88	NITCKNGHNCYOSKSTMSITD	CRGTGSSKYPNCAIKTSQKQYITVACBGNPYVPVHFD	147
		: :	: :	
QY	105	G	105	G
Db	148	G	148	G

RESULT 10				
RNP_PIG	STANDARD;	PRT;	124	AA.
ID	RNP_PIG	STANDARD;	PRT;	124
AC	P00671;			
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Ribonuclease pancreatic (EC 3.1.27.5)	(RNase 1)	(RNase A).	
DE	RNASE1 OR RNS1.			
OS	Sus scrofa (Pig).			
OC	Eukaryota; Metazoa;			
OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
OX	NCB1_TaxID=9823;			
RN	[1]			
RN	SEQUENCE.			
RP	MEDLINE=70104197; PubMed=5460946;			
RP	Jackson R.L., Hirs C.H.W.;			
RA	"The primary structure of porcine pancreatic ribonuclease. II. The			
RT	amino acid sequence of the reduced S-aminoethylated protein.";			
RT	J. Biol. Chem. 245:637-653(1970).			
RL	[2]			
RL	REVISION TO 2.			
RP	Wierenga R.K., Huizinga J.D., Gastra W., Welling G.W., Beintema J.J.;			
RP	"Affinity chromatography of porcine pancreatic ribonuclease and			
RT	reinvestigation of the N-terminal amino acid sequence.";			
RT	FEBS Lett. 31:181-185(1973).			
RL	[3]			
RP	DISULFIDE BONDS.			
RP	MEDLINE=70104198; PubMed=4904878;			
RA	Phelan J.J., Hirs C.H.W.;			
RT	"The primary structure of porcine pancreatic ribonuclease. 3. The			
RT	disulfide bonds.";			
RP	J. Biol. Chem. 245:654-661(1970).			
CC	-1- CATALYTIC ACTIVITY; Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Pancreas.			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR; A92071; NRPQ			
DR	HSP; P00656; ISRN.			
DR	InterPro; IPR001427; RNaseA.			
DR	Pfam; PF00074; rnasea; 1.			
DR	PRINTS; PR00794; RIBONUCLEASE.			
DR	ProDom; PD000535; RNaseA; 1.			
DR	SMART; SM00092; RNase_Pc; 1.			
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	DISULFID	26	84	
FT	DISULFID	40	95	
FT	DISULFID	58	110	
FT	DISULFID	65	72	
FT	ACT_SITE	12	12	
FT	ACT_SITE	41	41	
FT	ACT_SITE	119	119	
FT	CARBOHYD	21	21	
FT	CARBOHYD	34	34	
FT	CARBOHYD	76	76	

FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	N-LINKED (GLCNAC. . .).
FT	N-LINKED (GLCNAC. . .).
FT	N-LINKED (GLCNAC. . .).

RL	J. Biochem.	106:729-735 (1989).
CC	-I- CATALYTIC ACTIVITY:	Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2', 3'-cyclic phosphate intermediates.
CC	-II- SUBCELLULAR LOCATION:	Secreted.
CC	-I- SIMILARITY:	Belongs to the pancreatic ribonuclease family.
DR	HSP; JX0085;	JX0085.
DR	HSP; P13916;	1BCA.
DR	InterPro:	IPIR001427; RNaseA.
DR	Pfam;	PF00074; rnaseaA; 1.
DR	ProDom;	PD000535; RNaseA; 1.
DR	SMART;	SMO0092; RNase Pc; 1.
DR	PROSITE;	PS00127; RNASE PANCREATIC; 1.
KW	Hydrolase;	Nuclease; Endonuclease; Pyrirolidone carboxylic acid.
FT	MOD RES	1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	ACT SITE	10 10 BY SIMILARITY.
FT	ACT SITE	35 35 BY SIMILARITY.
FT	ACT SITE	104 104 BY SIMILARITY.
FT	DISULFD	19 72 BY SIMILARITY.
FT	DISULFD	34 82 BY SIMILARITY.
FT	DISULFD	52 97 BY SIMILARITY.
FT	DISULFD	94 111 PROBABLE.
SQ	SEQUENCE	111 AA; 12461 MW; D64BA72456C10788 CRC64;
Query Match 61.4%; Score 369; DB 1; Length 111;		
Best Local Similarity 65.5%; Pred. No. 6, 4e-33;		
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2		
Oy	2	NWATFOQRKIINTPLI-CNTIMDNNNYIVGGCKRVNFTFISSATFVKAICTGVI-NMNV 59 : : : : : : : : : :
Db	2	NWAKEKEGHIRSTSIDCNTIMDKAIYIVGGCKERNFTFISSDNVAICSGVSPDRKE 61 : : : : : : : : : :
Oy	60	LSTTRFQNLCTRTSITPRPCPYSRSTRTNVICVKENQYPVHFAGIGRC 109 : : : : : : : : : :
bB	62	LSTTSFKLNTCIROSITPRPCPYHSPDNNKICVKCEKQLPVHFGIGKC 111 : : : : : : : : : :

RESULT 4

RN30	RANPI		
ID	RN30	RANPI	STANDARD; PRT; 104 AA.
AC	P22069;		
DT	01-AUG-1991	(Rel. 19, Created)	
DT	01-FEB-1994	(Rel. 28, Last sequence update)	
DT	28-FEB-2003	(Rel. 41, Last annotation update)	
DE	P-30 protein	(EC 3.1.27.-) (Onconase).	
OS	Rana pipiens	(Northern leopard frog).	
OS	Eukaryota;	Metazoa;	Chordata;
OC	Amphibia;	Batrachia;	Anura;
OC	NCBI_TaxID=8404;		
OX	[1]		
RN	SEQUENCE.		
RP	TISSUE=Embryo;		
RC	MEDLINE=91093131;	PubMed=1985896;	
RA	Ardelt W., Mikulski S.M., Shogen K.;		
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens		
RT	oocytes and early embryos. Homology to pancreatic ribonucleases."		
RL	J. Biol. Chem. 266:245-251 (1991).		
RN	[2]		
RP	3D-STRUCTURE MODELING.		
RC	MEDLINE=93066156;	PubMed=1438177;	
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,		
RA	James M.N.G.;		
RT	"Comparative molecular modeling and crystallization of P-30 protein:		
RT	a novel antitumor protein of Rana pipiens oocytes and early		
RT	embryos."		
RL	Proteins 14:392-400 (1992).		
RN	[3]		
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).		
RC	MEDLINE=94166079;	PubMed=8120892;	
RA	Mosimann S.C., Ardelt W., James M.N.G.;		
RT	"Refined 1.7 A x-ray crystallographic structure of P-30 protein, an		
RT	amphibian ribonuclease with anti-tumor activity."		
RL	J. Mol. Biol. 236:1141-1153 (1994).		

CC	-1- FUNCTION: Basic protein with antiproliferative/cytotoxic activity against several tumor cell lines in vitro, as well as antitumor in vivo. It exhibits a ribonuclease-like activity against high molecular weight ribosomal RNA.
CC	-1- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR	PDB; IONC; 31-JAN-94.
DR	InterPro; IPR001427; RNaseA.
DR	Pfam; PF00074; RNaseA; 1.
DR	ProDom; PD000535; RNaseA; 1.
DR	SMART; SM00092; RNase_Pc; 1.
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR	Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW	Pyrrolidone carboxylic acid.
KW	MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT	ACT_SITE 10 10
FT	ACT_SITE 31 31
FT	ACT_SITE 97 97
FT	DISULFID 19 68
FT	DISULFID 30 75
FT	DISULFID 48 90
FT	DISULFID 87 104
FT	HELIX 3 10
FT	STRAND 11 12
FT	HELIX 19 22
FT	TURN 23 24
FT	TURN 26 30
FT	STRAND 33 38
FT	HELIX 41 45
FT	HELIX 46 48
FT	TURN 49 50
FT	STRAND 55 58
FT	STRAND 63 70
FT	TURN 74 75
FT	STRAND 77 84
FT	STRAND 86 91
FT	TURN 92 93
FT	TURN 94 101
SQ	SEQUENCE 104 AA; 22A753C2F9E566B4 CRC64;

Query Match 45.3%; Score 272.5; DB 1; Length 104;
 Best Local Similarity 49.1%; Pred. No. 1.4e-22;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy	2	NWAFQFKHIINT-PIICNTIMDNVIYVGQCKRVNTFTFISSATTVKAICTGVI--NMV 59
Db	2	DWLTFQKKHINTRDVDCNMSTNLF----HCKDKNTFYISRPVPKAIKGIASKV 57
Qy	60	LSITRFQINCTRTSITPRPCPSYSSRTETNYICVKENQVVPVHFAGIRC 109
Db	58	LTTSEFYLSDC---NVTSRPCKYKIKKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 5
 AN3 MOUSE
 ID _AN3 MOUSE STANDARD; PRT; 145 AA.
 AC P97802;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2) (EF-5).
 DE DE
 GN AN3 OR ANGL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX MEDLINE=97184476; PubMed=9032278;
 FT Xu X., Kamps M.P.;
 RT "E2a-Pbx1 induces aberrant expression of tissue-specific and

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:24:28 ; Search time 9.95475 Seconds

(without alignments)
575.375 Million cell updates/sec

Title: US-09-961-400-24

Perfect score: 601

Sequence: 1 SNWATFQKHINPIICNT.....ICVKCNQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	586.5	97.6	133	1 RNP_O RANCA	P11916 rana catesb
2	450	74.9	111	1 LECS RANCA	P18839 rana japoni
3	369	61.4	111	1 RNP_O RANCA	P14626 rana catesb
4	272.5	45.3	104	1 RNP_O RANCA	P22069 rana pipien
5	154.5	25.7	145	1 ANG_MOUSE	P97802 mus musculu
6	149.5	24.9	145	1 ANG_MOUSE	Q64438 mus musculu
7	135.5	22.5	124	1 RNP_BALAC	P00673 balaenopter
8	135.5	22.5	145	1 ANG_MOUSE	P21570 mus musculu
9	133.5	22.2	167	1 RNP_O BOVIN	P39873 bos taurus
10	132.5	22.0	124	1 RNP_PIG	P00671 sus scrofa
11	128.5	21.4	151	1 RNP_O CAPCA	P79351 capreolus c
12	127.5	21.2	123	1 ANG2 BOVIN	P80929 bos taurus
13	127.5	21.2	141	1 RNP_O GIRCA	Q29542 giraffa cam
14	127.5	21.2	151	1 RNP_O AXIPR	P87350 axis porcin
15	126.5	21.0	119	1 RNP_IGUIG	P80287 iguana igua
16	126.5	21.0	146	1 ANG_CERAE	Q8wn66 cercopithec
17	126.5	21.0	146	1 ANG_MOTA	Q8wn65 miopithecus
18	125	20.8	146	1 ANG_SAISCP	Q8wn60 saimiri sci
19	123.5	20.5	143	1 RNP_O SHEEP	Q29543 ovis aries
20	122.5	20.4	124	1 RNP_O ANTM	P00668 antilocapra
21	122	20.3	122	1 RNP_O MACRU	P00686 macropus ru
22	120.5	20.0	128	1 RNP_O MYOCO	P00676 myocastor c
23	120.5	20.0	147	1 ANG_PONPY	Q8wn67 pongo pygma
24	120.5	20.0	149	1 RNP_MOUSE	P00683 mus musculu
25	120	20.0	146	1 ANG_O ACTTR	Q8wn61 aotus trivi
26	119.5	19.9	123	1 ANG_PIG	P31346 sus scrofa
27	118.5	19.7	128	1 RNP_O CAVPO	P00679 cavia porce
28	117.5	19.6	146	1 ANG_SAGOE	Q8wn62 saguinus oe
29	117.5	19.6	128	1 RNP_HORSE	P00674 equus caball
30	116.5	19.4	124	1 RNP_CAMDR	P00670 camelus dro
31	116.5	19.4	128	1 RNP_PROGU	P04059 proechinus
32	115.5	19.2	119	1 RNP_O BOVIN	P15467 bos taurus
33	115.5	19.2	146	1 ANG_O MACMU	Q8wn63 macaca mula

RESULT 1
RNP_O RANCA
ID RNP_O RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
ON NCBI_TaxID=8400;
RX MEDLINE=87299649; PubMed=3304421;
TX TISSUE=Liver;
RP SEQUENCE FROM N.A.
RC TISSUE=Egg;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RA "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity";
RL J. Biol. Chem. 273:6395-6401(1998).
[2]
RN SEQUENCE OF 23-133.
TX TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RA "Amino acid sequence of sialic acid binding lectin from frog (Rana
RL catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
[3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RA "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RL catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
[4]
RP CHARACTERIZATION.
TX TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RA "Ribonuclease activity of sialic acid-binding lectin from Rana
RL catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
[5]
RN STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RA "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RT J. Mol. Biol. 283:231-244(1998).
CC !- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

34 114 19.0 148 1 ANGI_BOVIN P10152 bos taurus
35 113.5 18.9 124 1 RNP_RANTA P00666 rangifer ta
36 113.5 18.9 125 1 ANGI_RABIT P31347 oryctolagus
37 113.5 18.9 146 1 ANGI_PAPHA Q8wn64 papio hamad
38 113 18.8 147 1 ANGI_HUMAN P03950 homo sapien
39 113 18.8 147 1 ANGI_PANTR Q8wn68 pan troglod
40 112.5 18.7 124 1 RNP_CAPCA P00664 capreolus c
41 112.5 18.7 124 1 RNP_GIRCA P00662 giraffa cam
42 112.5 18.7 148 1 RNP_MOUSE Q9jjh1 mus musculu
43 111.5 18.6 130 1 RNP_CRILO P24717 cricetus
44 111.5 18.6 147 1 RNP4_RAT Q55004 rattus norv
45 111.5 18.6 149 1 RNP_ACOCA Q9wt55 acomys cahi

Search completed: May 11, 2004, 14:37:08
Job time : 14.4389 secs

J. Mol. Evol. 13, 305-316, 1979

A>Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship bet

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BEI>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.4%; Score 122.5; DB 1; Length 124;

Best Local Similarity 30.3%; Pred. No. 3.e-05;

Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY 4 ATPOQRHINPTI-----ICNTIMDNNIYVGQCKRVNTFISSATTVKAICGVNIM 57

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QY 2 NWATFOQKHINTP-IICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 NWAKFQKHINTSINCNTIMDKSIYVGGQCKERNFTFISSATTVAICTGSGASTNRV 61
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 62 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENRLPVHFAGIGRC 111

RESULT 3
JKX0085
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.4%; Score 369; DB 2; Length 111;
Best Local Similarity 65.5%; Pred. No. 9,6e-30;
Matches 72; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 NWATFOQKHINTP-II-CNTIMDNNIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 NWAKFQKHINTSINCNTIMDKSIYVGGQCKERNFTFISSATTVAICTGSGASTNRV 61
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 62 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENRLPVHFAGIGRC 111

RESULT 4
A39035
Ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 45.3%; Score 272.5; DB 2; Length 104;
Best Local Similarity 49.1%; Pred. No. 3.5e-20;
Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 NWATFOQKHINTP-IICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGV-INNV 59
DB 2 DWLTFQKHINTDVRDVCNDIMTNLF----HCKDKNTFIYSRPEPVKAICKGLIASKNV 57
QY 60 LSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 58 LTTSEFYLSDC---NVTSRPKYKLLKSNKTKFCVTCENQAPVHFVGVGSC 104

RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale

```

```

N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1994 #sequence_revision 24-Apr-1994 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.5%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 6 FQOKHII-----NTPICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNV 59
DB 8 FQOKHII-----NTPICNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNV 59
QY 60 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHF 103
DB 64 LCKNGRINCYESNSTMTIDCRQTGSSKYPNCAYKTSQKXKHIIVACGPNYPVHF 120

RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U2516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.5%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 33 CKRVNTFISSATTVAICTGVINNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 87
DB 63 CKRVNTFIHGKNIRKAIKANGSPYRENLKMSPPQVTTCKTGSGPRPCQYRASAG 122
QY 88 TNYICVKCENQYPVHF 103
DB 123 FRHVTIACENGLPVHF 138

RESULT 7

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:31:13 ; Search time 13.4389 Seconds

(without alignments)
787.345 Million cell updates/sec

Title: US-09-961-400-24

Perfect score: 601

Sequence: 1 SNWTFQOKHIINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	586.5	97.6	111	2 A27121	ribonuclease-relat
2	450	74.9	111	1 JX0120	ribonuclease-relat
3	369	61.4	111	2 JX0085	pancreatic ribonuc
4	272.5	45.3	104	2 A39035	ribonuclease-relat
5	135.5	22.5	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.5	145	1 A35932	angiogenin precurs
7	133.5	22.2	167	2 S20066	pancreatic-type ri
8	132.5	22.0	124	1 NRPG	pancreatic ribonuc
9	126.5	21.0	119	2 S41111	pancreatic ribonuc
10	122.5	20.4	124	1 NRPRH	pancreatic ribonuc
11	122	20.3	122	1 NRKGR	pancreatic ribonuc
12	120.5	20.0	128	1 NRKU	pancreatic ribonuc
13	120.5	20.0	149	1 NRMS	pancreatic ribonuc
14	119.5	19.9	123	1 A43825	angiogenin - p19
15	118.5	19.7	128	1 NRGPB	pancreatic ribonuc
16	117.5	19.6	128	1 NRHO	pancreatic ribonuc
17	116.5	19.4	124	1 NRKM	pancreatic ribonuc
18	116.5	19.4	124	1 NRKM	pancreatic ribonuc
19	116.5	19.4	124	1 NRKM	pancreatic ribonuc
20	116.5	19.4	128	1 NRKS	pancreatic ribonuc
21	114.5	19.1	124	2 S08549	ribonuclease - dom
22	114	19.0	125	1 A32474	angiogenin [valida
23	113.5	18.9	124	1 NRDEN	pancreatic ribonuc
24	113.5	18.9	125	1 B43825	angiogenin - rabbi
25	113	18.8	147	1 NRHUG	angiogenin precurs
26	112.5	18.7	124	1 NRGF	pancreatic ribonuc
27	112.5	18.7	124	1 NRDEO	pancreatic ribonuc
28	111.5	18.6	130	2 S22808	pancreatic ribonuc
29	110.5	18.4	124	1 NRBOB	pancreatic ribonuc

30	110.5	18.4	124	1 NRWB	pancreatic ribonuc
31	110.5	18.4	124	1 NREKN	pancreatic ribonuc
32	110.5	18.4	124	2 S07141	pancreatic ribonuc
33	110.5	18.4	150	1 NRBO	pancreatic ribonuc
34	110.5	18.4	158	2 I61900	eosinophil-derived
35	109.5	18.2	124	1 NRSH	pancreatic ribonuc
36	108.5	18.1	119	2 JX0115	pancreatic ribonuc
37	108.5	18.1	124	1 NRCH	pancreatic ribonuc
38	108.5	18.1	124	1 NRRT	pancreatic ribonuc
39	106.5	17.7	124	1 NRHP	pancreatic ribonuc
40	106.5	17.7	125	4 A47498	seminal ribonuclea
41	106.5	17.7	150	1 NREOS	pancreatic ribonuc
42	104.5	17.4	124	1 NRGN	pancreatic ribonuc
43	104.5	17.4	124	1 NRDEF	pancreatic ribonuc
44	104	17.3	125	2 S04503	pancreatic ribonuc
45	103.5	17.2	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121

ribonuclease-related sialic acid-binding lectin - bullfrog

C;Species: Rana catesbeiana (bullfrog)

C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C;Accession: A27121

R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi

Biochemistry 26, 2189-2194, 1987

A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A;Reference number: A27121; MUID:87299649; PMID:3304421

A;Accession: A27121

A;Molecule type: protein

A;Residues: 1-111 <PII>

C;Superfamily: pancreatic ribonuclease

C;Keywords: lectin

Query Match 97.6%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.3e-51;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 2 NWATFOOKHIINTPII-CNTIMDNIIYVGCKRVNTFTIISATTVAICTGVINNNVL 60
Db 2 NWATFOOKHIINTPII-CNTIMDNIIYVGCKRVNTFTIISATTVAICTGVINNNVL 61

Qy 61 STTRFQNTCTRTSITPRCPYSRSTETNYICVKCENQYPVHFAGIGRCP 110

Db 62 STTRFQNTCTRTSITPRCPYSRSTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120

ribonuclease-related sialic acid-binding lectin - Japanese frog

C;Species: Rana japonica (Japanese frog)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C;Accession: JX0120

R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi

J. Biochem. 108, 139-143, 1990

A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A;Reference number: JX0120; MUID:91035319; PMID:2229005

A;Accession: JX0120

A;Molecule type: protein

A;Residues: 1-111 <KAM>

A;Experimental source: egg

C;Superfamily: pancreatic ribonuclease

C;Keywords: lectin; pyroglyutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match

74.9%; Score 450; DB 1; Length 111;

Best Local Similarity 78.2%; Pred. No. 8.6e-38;

Matches 86; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

KW		recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XW		autoimmune disease.
XX	XX	
OS	OS	Rana pipiens.
OS	OS	Synthetic.
XX	XX	
FH		Key Location/Qualifiers
FT	FT	Misc-difference 1
FT	FT	/note= "Met not found in wild type RaPLr1"
XX	XX	
PN	PN	WO9950398-A2.
XX	XX	
PD	PD	07-OCT-1999.
XX	XX	
PF	PF	26-MAR-1999; 99WO-US006641.
XX	XX	
PR	PR	27-MAR-1998; 98US-0079751P.
XX	XX	
PA	PA	(USH) US DEPT HEALTH & HUMAN SERVICES.
XX	XX	
PI	PI	Rybak SM, Newton DL;
XX	XX	
DR	DR	WPI; 1999-610847/52.
DR	DR	N-PSDB; AAZ08126.
XX	XX	
PT	PT	New recombinant ribonucleases, used for killing target cells, e.g. for
PT	PT	treating cancers, viral infections or autoimmune diseases.
XX	XX	
PS	PS	Claim 34; Page 57; 7lpp; English.
XX	XX	
CC	CC	The present sequence is a recombinant Rana pipiens ribonuclease (RaPLr1)
CC	CC	protein with Met at position 1. Carboxy terminal end of recombinant
CC	CC	RaPLr1 has a covalently bound ligand binding moiety, which can be a IL2
CC	CC	antibody directed against CD22 on cancerous B cells or human chorionic
CC	CC	gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC	CC	ribonucleases can be expressed in bacteria without an N-terminal
CC	CC	methionine due to the presence of a signal peptide that is cleaved by
CC	CC	bacteria. The soluble expression of ribonuclease allows the proteins to
CC	CC	be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC	CC	proteins. They can be used for treatment of cancer and autoimmune
CC	CC	diseases
XX	XX	
SQ	SQ	Sequence 105 AA;
		Query Match 46.0%; Score 276.5; DB 2; Length 105;
		Best Local Similarity 49.1%; Pred.No.1.1e-23;
		Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4
QY	2	NWATFQQRIINT-PIICNTIMNNIYVGQCKRVNFIISATTVAICTGVI--NMNV 59
		: :: :: : :: : :: : :: : :: : :: :
Db	3	DWLTFQKXHLNTRDVCNNIMSTNLF---HCKDKNTFYSRPEPVKAICKGIILAKNV 58
		: :: :: : :: : :: : :: : :: : :: :
QY	60	LSTRFQNTCRITSITRPDPYSRTEINYICVKENCQYPVHFAGIGRC 109
		: :: :: : :: : :: : :: : :: : :: :
Db	59	LTTSEFYLSDC---NVTSRPCYKLKSTNTFCVTENQAPVHFVGVGHG 105
		: :: :: : :: : :: : :: : :: : :: :
RESULT 13		
AAW35118	ID	AAW35118 standard; protein; 112 AA.
XX	XX	
AC	AC	AAW35118;
XX	XX	
DT	20-APR-1998	(first entry)
XX	XX	
DE		R. pipiens recombinant RNase protein NLSMetSerrOnc.
KW		RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
KW		tumour cell growth; frog.
XX	XX	
OS	OS	Rana pipiens.
XX	XX	
PN	PN	WO9731116-A2.

ID AAY28871 standard; protein; 105 AA.
 XX AC AAY28871;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met (-1) RaPLR1 GlnSer amino acid sequence.
 XX KW Recombinant Met (-1) Rana pipiens ribonuclease GlnSer; RaPLR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease; RNase.
 XX OS Rana pipiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 FT
 XX PN W09950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08129.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 34; Page 61; 71pp; English.
 XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1 and Gln28er. Carboxy terminal end of
 CC recombinant RaPLR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX SQ Sequence 105 AA;
 Query Match 46.7%; Score 280.5; DB 2; Length 105;
 Best Local Similarity 49.5%; Pred. No. 3.9e-24;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 1 SNWATFQOKHIINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NMN 58
 DB 2 SDWLTFFQKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57
 QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
 DB 58 VLTTFEFLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 RESULT 11
 AAY28865
 ID AAY28865 standard; protein; 104 AA.

XX AAY28865;
 XX AC 25-JAN-2000 (first entry)
 XX DE Rana pipiens liver ribonuclease (RaPLR1).
 XX KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
 KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX OS Rana pipiens.
 XX PN W09950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR 27-MAR-1998; 98US-0079751P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08124.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX PS Claim 1; Page 55; 71pp; English.
 XX CC The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
 CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
 CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
 CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 CC without an N-terminal methionine due to the presence of a signal peptide
 CC that is cleaved by bacteria. The soluble expression of ribonuclease
 CC allows the proteins to be fused in-frame with ligand binding moieties to
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 CC and autoimmune diseases
 XX SQ Sequence 104 AA;
 Query Match 46.0%; Score 276.5; DB 2; Length 104;
 Best Local Similarity 49.1%; Pred. No. 1.1e-23;
 Matches 54; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 2 NWATFQOKHIINT-PIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVI-NMN 59
 DB 2 DWLTFQKHLNTRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 57
 QY 60 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
 DB 58 LTTSEFLSDC---NVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 RESULT 12
 AAY28867
 ID AAY28867 standard; protein; 105 AA.
 XX AC AAY28867;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met (-1) RaPLR1.
 XX KW Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

```

CC (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ Sequence 111 AA;

Query Match          97.6%; Score 586.5; DB 2; Length 111;
Best Local Similarity 99.1%; Pred. No. 3.8e-59;
Matches 109; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 NWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVNL 60
DB 2 NWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVNL 61

QY 61 STTRFQNLNCTRTSIITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 110
DB 62 STTRFQNLNCTRTSIITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111

RESULT 8
AAW06544
ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DT 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN W09639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Ardelt WJ;
XX
DR WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX
CC The present sequence is a specifically claimed example of an antitumour
CC protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match          47.0%; Score 282.5; DB 2; Length 104;
Best Local Similarity 50.0%; Pred. No. 2.3e-24;
Matches 55; Conservative 15; Mismatches 31; Indels 9; Gaps 4;

QY 2 NWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMNV 59
DB 2 DWLTFQKHINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNV 57

QY 60 LSTTRFQNLNCTRTSIITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 109
DB 58 LTISEFYLSDC----NVTSPCKYKLKSTNFCVTCENQAPVHFVGVGRC 104

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RESULT 9
AAY28870
ID AAY28870 standard; protein; 104 AA.
XX
AC AAY28870;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RapiR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Rana pipiens ribonuclease; RapiR1 Gln1Ser; covalently bound;
KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
KW autoimmune disease.
XX
OS Rana pipiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
XX
PN W09550398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
DR N-PSDB; AAZ08128.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 34; Page 60; 71pp; English.
XX
CC The present sequence is a recombinant Rana pipiens ribonuclease (RapiR1)
CC protein with Gln1Ser. Carboxy terminal end of recombinant RapiR1 has a
CC covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases
XX
SQ Sequence 104 AA;

Query Match          46.7%; Score 280.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 3.8e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 SNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 58
DB 1 SDWLTFQKHINTRDVDCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKNV 56

QY 59 VLSTTRFQNLNCTRTSIITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 109
DB 57 VLTTSEFYLSDC----NVTSPCKYKLKSTNFCVTCENQAPVHFVGVGHC 104

RESULT 10
AAY28871

```


QY 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61
 DB 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61
 QY 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
 AAY28876
 ID AAY28876 standard; protein; 111 AA.
 XX AC
 XX AC
 XX DT
 XX DT
 XX DE
 XX DE
 XX KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6 protein.
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX OS Rana catesbeiana.
 OS Synthetic.
 XX FH
 XX FT Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
 FT FT
 XX KW WO9950398-A2.
 XX PN
 XX XX
 XX PD 07-OCT-1999.
 XX XX
 XX PF 26-MAR-1999; 99WO-US006641.
 XX PR
 XX PA 27-MAR-1998; 98US-0079751P.
 XX XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Rybak SM, Newton DL;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08133.
 XX XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 XX XX
 XX PS Claim 22; Page 66; 71pp; English.
 XX XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 XX diseases
 XX SQ Sequence 111 AA;

Query Match 98.3%; Score 591; DB 2; Length 111;
 Best Local Similarity 98.2%; Pred. No 1.2e-59;
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 61
 DB 3 NWATFQOKHIINTPIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINMNVLS 62
 QY 62 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 63 TTRFOLNTCTRTSTITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
 AAY33321
 ID AAY33321 standard; protein; 111 AA.
 XX AC
 XX AC
 XX DT 29-NOV-1999 (first entry)
 XX DT
 XX DE Frog lectin protein fragment.
 XX DE
 XX KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
 KW heavy chain; cell surface marker; treatment; tumor; viral infection;
 KW parasite infection; immune dysfunctional cell; autoimmune disease;
 KW contraceptive; cell separation; transplantation; bone marrow ablation;
 KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
 XX OS Rana catesbeiana.
 OS US9555073-A.
 XX PN
 XX PD 21-SEP-1999.
 XX XX
 XX PF 09-JUL-1997; 97US-00891848.
 XX PR 20-APR-1990; 90US-00510696.
 PR 22-OCT-1991; 91US-00779195.
 PR 04-FEB-1993; 93US-00014082.
 PR 22-SEP-1993; 93US-00125462.
 XX XX
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX XX
 XX PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
 XX XX
 XX DR WPI; 1999-560488/47.
 XX XX
 XX PT Recombinantly fused pancreatic RNase-targeting proteins useful for
 PT treating tumors, infections, immune or autoimmune disorders and as a
 PT contraceptive.
 XX XX
 XX PS Example 3; Fig 19; 47pp; English.
 XX XX
 CC This invention describes a novel nucleic acid construct comprising
 CC sequences encoding functional pancreatic RNase and a second protein
 CC (preferably the light and heavy chains of an antibody) which binds a
 CC specific cell surface marker on a target cell and functions as a
 CC cytotoxic agent. The products can be used for selectively killing cells
 CC expressing a specific surface marker. They can be used for treating
 CC tumors or infected cells (e.g. cells infected by viruses (especially
 CC latent or chronic virus infections, such as human immunodeficiency virus
 CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
 CC II), hepatitis viruses (B, non-A non-B, and delta), herpes zoster,
 CC cytomegalovirus) and cells infected with parasites (such as the malaria
 CC parasite)). They can also be used for treating immune dysfunctional cells
 CC in immune and autoimmune diseases. Additionally, they may be used as
 CC contraceptives. Finally they can also be used for cell separation in
 CC vitro by selectively killing unwanted types of cells (e.g. in bone
 CC marrow) prior to transplantation into a patient undergoing marrow
 CC ablation by radiation or for killing leukemia cells or T-cells that would
 CC cause graft-versus-host disease. This sequence represents a bullfrog

Query Match 99.3%; Score 597; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.4e-60; Indels 0; Gaps 0;
 Matches 109; Conservative 0; Mismatches 0;

QY 2 NWATFQQRHINTPIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNVL 61
 DB 2 NWATFQQRHINTPIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNVL 61
 QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
 DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110

RESULT 4
 AAY28873
 ID AAY28873 standard; protein; 111 AA.

AC AAY28873;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant Met (-1) RaCOR1.
 XX Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; IL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.

OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT

PN WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08131.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 63; 71pp; English.
 XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a IL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 111 AA;

Query Match 99.3%; Score 597; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2.4e-60;

Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQQRHINTPIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNVL 61
 DB 3 NWATFQQRHINTPIICNTIMDNNIYVGGQCKRVNTFISSATVKAICTGVINNVL 62
 QY 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
 DB 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 111

RESULT 5
 AAY28874
 ID AAY28874 standard; protein; 110 AA.

AC AAY28874;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
 XX Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
 KW RaCOR1 Met22Leu Met57Leu; IL2 antibody; ligand binding moiety; CD22;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 22 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"
 FT

XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08132.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 64; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety, or
 CC which can be a IL2 antibody directed against CD22 on cancerous B cells, or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 98.3%; Score 591; DB 2; Length 110;
 Best Local Similarity 98.2%; Pred. No. 1.1e-59;
 Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 601; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 8.2e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNWATFQOKHIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 60
 Db 1 SNWATFQOKHIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 60
 QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 2
 AAY28878
 ID AAY28878 standard; protein; 111 AA.
 XX
 AC AAY28878;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.

XX Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW CD22; RNase; autoimmune disease.

XX Rana catesbeiana.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 FT

XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08135.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 68; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana ribonuclease
 CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
 CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-

CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX
 SQ Sequence 111 AA;

Query Match 100.0%; Score 601; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 8.3e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNWATFQOKHIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 60
 Db 2 SNWATFQOKHIINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 61
 QY 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 Db 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
 RAY28872
 ID AAY28872 standard; protein; 110 AA.
 XX
 AC AAY28872;
 XX
 DT 25-JAN-2000 (first entry)
 XX

DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

XX Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.

XX Rana catesbeiana.
 OS Synthetic.

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08130.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 62; 71pp; English.

XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's Sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 110 AA;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 11, 2004, 14:23:43 ; Search time 50.2715 Seconds
(without alignments)
618.248 Million cell updates/sec

Title: US-09-961-400-24
Perfect score: 601
Sequence: 1 SNWATFOQKHINTPLICNT.....ICVKCNQYVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 29Jan04:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601	100.0	110	2	AAY28877 Recombina
2	601	100.0	111	2	AAY28878 Recombina
3	597	99.3	110	2	AAY28872 Rana cate
4	597	99.3	111	2	AAY28873 Recombina
5	591	98.3	110	2	AAY28874 Recombina
6	591	98.3	111	2	AAY28876 Recombina
7	586.5	97.6	111	2	AAY33321 Frog lect
8	282.5	47.0	104	2	Aaw06544 Antitumou
9	280.5	46.7	104	2	AAY28870 Recombina
10	280.5	46.7	105	2	AAY28871 Recombina
11	276.5	46.0	104	2	AAY28865 Rana pipi
12	276.5	46.0	105	2	AAY28867 Recombina
13	276.5	46.0	112	2	Aaw35118 R. pipien
14	276.5	46.0	127	2	AAY28879 Rana pipi
15	276.5	46.0	251	2	Aaw35134 R. pipien
16	276.5	46.0	254	2	Aaw35135 R. pipien
17	276.5	46.0	355	2	Aaw35133 R. pipien
18	276.5	46.0	355	2	Aaw35129 R. pipien
19	276.5	46.0	366	2	Aaw35132 R. pipien
20	273.5	45.5	104	2	AAY28866 Recombina
21	273.5	45.5	105	2	AAY28869 Recombina
22	272.5	45.3	104	2	AAR12344 Protein w
23	272.5	45.3	104	2	AAR47303 ONCONASE
24	272.5	45.3	104	2	Aaw00736 Protein d
25	272.5	45.3	104	2	Aaw14065 Oncogene

ALIGNMENTS

RESULT 1

AAY28877
ID AAY28877 standard; protein; 110 AA.
XX
AC AAY28877;
XX
DT 25-JAN-2000 (first entry)
DE Recombinant RACOR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Rana catesbeiana oocyte ribonuclease; RACOR1 Gln1Ser; CD22;
covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
cancer; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
FT
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
DR N-PSDB; AAZ08134.
PT New recombinant ribonucleases, used for killing target cells, e.g. for
treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 67; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
ribonuclease (RACOR1) protein with Gln1Ser. Carboxy terminal end of
recombinant RACOR1 has a covalently bound ligand binding moiety, which
can be a LL2 antibody directed against CD22 on cancerous B cells or human
chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

26	272.5	45.3	104	2	AAW06543
27	272.5	45.3	104	2	AAW30301
28	272.5	45.3	104	2	AAW88233
29	272.5	45.3	104	2	AAY33322 Frog onco
30	272.5	45.3	104	4	AAB31666 Amino aci
31	272.5	45.3	104	5	ABG32850 Northern
32	272.5	45.3	105	2	AAW35123 R. pipien
33	272.5	45.3	105	2	AAY39400 Recombina
34	272.5	45.3	106	2	AAW35122 R. pipien
35	272.5	45.3	107	2	AAW35117 R. pipien
36	272.5	45.3	355	2	AAW35125 R. pipien
37	272.5	45.3	358	2	AAW35130 R. pipien
38	272.5	45.3	379	2	AAW35126 R. pipien
39	271.5	45.2	105	2	AAW35116 R. pipien
40	269.5	44.8	104	2	AAW30302 Recombina
41	267.5	44.5	104	4	AAB31667 Amino aci
42	267.5	44.5	104	5	ABG31617 Northern
43	267.5	44.5	105	2	AAW35115 R. pipien
44	267.5	44.5	358	2	AAW35127 R. pipien
45	267.5	44.5	365	2	AAW35131 R. pipien


```

RA Beintema J.J.;
RT "secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL; Y11670; CAA72368.1; -.
CC HSP; P00656; ISRN.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACT SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; 16819 MW; E95F3757FFC5B233 CRC64;

Query Match 20.4%; Score 123.5; DB 1; Length 151;
Best Local Similarity 29.8%; Pred. No. 2.2e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

Qy 5 ATFOQKH-----INTPICNTILDNNIYVGQCKRVNTFLISSATTVKAITGVINL 58
Db 6 AKFRQHMADAGSSSGNSGNYCNQMRR-RMTHGRCKPVNTFVHESLDSVKAACS---QK 61

Qy 59 NVL-----STTRFLNTCTRTSITPRP-CFYSSRTETNYICVKE-NQY-PVHFA 105
Db 62 NITCKNGQPNCVQSNSTWNITDCRETGSSKYENCAYKTSQKQYITVACEGNPYVPVHFD 121

Qy 106 G 106
Db 122 G 122

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Search completed: May 7, 2004, 21:53:06
Job time : 5.60711 secs


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DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gaastera W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661 (1970).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A92071; NRPG.
DR HSHP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT ACT SITE 12 12
FT ACT SITE 12 12
FT ACT SITE 41 41
FT ACT SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT CARBOHYD 76 76
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE1411845 CRC64;

Query Match
Best Local Similarity 21.4%; Score 129.5; DB 1; Length 124;
Matches 35; Conservative 20; Mismatches 4; Indels 17; Gaps 6;

QY 7 PQKH-----INTPICTLNNIYVGGCKRVNTFISSATTVKAICTGV-INLN 59
Db 8 FQHQHMDPDSSSSNSNYCNLMMSRR-NWTQGRCKFNTFVHESLADYQAVCSQINVCK 66
QY 60 VLSITRFPNT-----CTRSITPRP-CPTSSRTETNYICVKCNQ--YVPHF 104
Db 67 NGQTCYOSNTMHTDCROTGSSKYPNCAYKASQEQKHIIIVACEGPPVPHF 120

RESULT 10
ENR_BOVIN
ID _RNR_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN BRN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92093604; PubMed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmieri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT and its expression in different regions of the brain.";
RL Nucleic Acids Res. 19:6469-6474 (1991).
RN [2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RC TISSUE=Brain;
RX MEDLINE=89214015; PubMed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain.";
RL J. Biochem. 104:939-945 (1988).
RN [3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species.";
RL J. Mol. Evol. 41:850-858 (1995).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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EMBL; X59767; CAA42439.1; -.
EMBL; S81744; AAB36138.1; -.
PIR; S20066; S20066.
HSHP; P00656; 2RNS.
GlycoSuiteDB; P39873; -.
InterPro; IPR001427; RNaseA.
Pfam; PF00074; RNaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNaseA; 1.
PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT SITE 38 38 BY SIMILARITY.
FT ACT SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC3FC459 CRC64;

Query Match
Best Local Similarity 21.4%; Score 129.5; DB 1; Length 167;
Matches 30.6%; Pred. No. 5.6e-07;

```

RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Kraywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiotensins: discernment of functionally important residues and
 RT regions.";
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -1- FUNCTION: May function as a tRNA-specific ribonuclease that binds
 CC to actin on the surface of endothelial cells; once bound,
 CC angiotensin is endocytosed and translocated to the nucleus, thereby
 CC promoting the endothelial invasiveness necessary for blood vessel
 CC formation. Angiotensin induces vascularization of normal and
 CC malignant tissues. Abolishes protein synthesis by specifically
 CC hydrolyzing cellular tRNAs.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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 CC or send an email to license@isb-sib.ch).
 CC ENBL; U22516; AAA91366.1; --
 DR ENBL; BC055355; AAH55355.1; --
 DR PIR; A35932; A35932.
 DR HSP; P03950; 1A4Y.
 DR MGD; MGI:88022; Ang.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 145
 FT MOD_RES 25 25
 FT FT PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 137 137
 FT ACT_SITE 104 104
 FT DISULFID 50 104
 FT DISULFID 63 115
 FT DISULFID 81 130
 FT DISULFID 81 130
 SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
 Query Match 22.6%; Score 136.5; DB 1; Length 145;
 Best Local Similarity 40.3%; Pred. No. 8.4e-08;
 Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;
 QY 34 CKRVNTFTLISSATTVKAICTG-----VINLVNLTTRFQNTCTRTSITPR-PCPYSSRT 87

Db 63 CKQVNTFHGNKSNKAIKANGSPYRENLR-MKSPFQVTTCKTGSPRPCCOYRASA 121
 QY 88 ETNYICVKCNQYPVHF 104
 Db 122 GFRHWIACENGLPVHF 138
 RESULT 8
 ID_RNP_BALAC
 AC P00673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaenopteridae; Balaenoptera.
 OX NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RT ribonuclease.";
 RL Biochem. J. 157:317-323(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Pancreas.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR; A00818; NRWHK.
 DR HSP; P00656; 1SRN.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT ACT_SITE 41 41
 FT ACT_SITE 119 119
 FT CARBOHYD 76 76
 SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;
 Query Match 21.7%; Score 131.5; DB 1; Length 124;
 Best Local Similarity 32.5%; Pred. No. 2.5e-07;
 Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;
 QY 7 FQKXHI-----NTPICNTILDNNIYVGGCKRVNTFTLISSATTVKAICTGVINLV 60
 Db 8 FQGHMDSGNSFGNNPNYCNQMMRR-KMTGCRKPVNTFVHESLEDYKAVCS---QKNV 63
 QY 61 L-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKCE-NOY-PVHF 104
 Db 64 LCKNGRTNVCYESNSTMHITDCRTGSSKYPNCAYKISQKXKHIIVACGPNFVPVHF 120
 RESULT 9
 ID_RNP_PIG
 AC P00671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

CC residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)
 CC as substrates, and prefers the former. The S-lectins in frog eggs
 CC may be involved in the fertilization and development of the frog
 CC embryo. This lectin agglutinates various animal cells, including
 CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
 CC human origin. It is cytotoxic against several tumor cells.
 CC
 CC -!- SUBUNIT: Monomer.
 CC
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF039104; AAD10702.1; -.
 CC PIR; A27121; A27121.
 CC PDB; 1BC4; 28-OCT-98.
 CC PDB; 1M07; 21-JAN-03.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
 CC Signal; Pyrolidone carboxylic acid.
 CC FT SIGNAL 1 22
 CC FT CHAIN 23 133 RIBONUCLEASE, OOCYTES.
 CC FT MOD_RES 23 23 PYRROLIDONE CARBOXYLIC ACID.
 CC FT ACT_SITE 32 32
 CC FT ACT_SITE 57 57
 CC FT ACT_SITE 125 125
 CC FT DISULFID 41 93
 CC FT DISULFID 56 103
 CC FT DISULFID 74 118
 CC FT DISULFID 115 132
 CC FT DISULFID 25 32
 CC FT HELIX 41 45
 CC FT TURN 48 49
 CC FT STRAND 59 63
 CC FT HELIX 67 73
 CC FT TURN 74 74
 CC FT STRAND 79 84
 CC FT STRAND 90 95
 CC FT STRAND 105 110
 CC FT STRAND 114 119
 CC FT TURN 120 121
 CC FT STRAND 122 129
 CC FT STRAND 133 133
 CC SQ SEQUENCE 133 AA; A7D62594F7D16F0C CRC64;
 CC
 CC Query Match 96.8%; Score 585.5; DB 1; Length 133;
 CC Best Local Similarity 97.3%; Pred. No. 3.2e-56;
 CC Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
 CC
 CC QY 2 QNWATFOQKHINTP-II-CNTILDNNIYVGGQCKRVNTFISSATTYKATCTGVINLV 60
 CC Db 23 QNWATFOQKHINTPINCNTIMDNNIYVGGQCKRVNTFISSATTYKATCTGVINLV 82
 CC
 CC QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 CC Db 83 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133
 CC
 CC RESULT 2
 CC LECS_RANJA STANDARD; PRT; 111 AA.
 CC ID LECS_RANJA
 CC AC P18839;
 CC DT 01-NOV-1990 (Rel. 16, Created)
 CC DT 01-PEB-1994 (Rel. 28, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Sialic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddy frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]
 RP SEQUENCE, AND DISULFIDE BONDS.
 RC TISSUE=EGG;
 RX MEDLINE=9105319; PubMed=2229005;
 RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
 RA Takayanagi Y., Titani K.;
 RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
 RT eggs.";
 RL J. Biochem. 108:139-143(1990).
 CC -!- FUNCTION: The S-lectins in frog eggs may be involved in the
 CC fertilization and development of the frog embryo. This lectin
 CC preferentially agglutinate a large variety of tumor cells, but it
 CC does not agglutinate non-transformed cells and erythrocytes.
 CC
 CC -!- SUBUNIT: Monomer.
 CC
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
 CC PIR; JX0120; JX0120.
 CC HSSP; P11916; 1BC4.
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
 CC Pyrolidone carboxylic acid.
 CC FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 CC FT ACT_SITE 10 10
 CC FT ACT_SITE 35 35
 CC FT ACT_SITE 104 104
 CC FT DISULFID 19 72
 CC FT DISULFID 34 82
 CC FT DISULFID 52 97
 CC FT DISULFID 94 111
 CC SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;
 CC
 CC Query Match 74.5%; Score 451; DB 1; Length 111;
 CC Best Local Similarity 77.5%; Pred. No. 8.1e-42;
 CC Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;
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 CC QY 2 QNWATFOQKHINTP-II-CNTILDNNIYVGGQCKRVNTFISSATTYKATCTGV-INLV 59
 CC Db 1 QNWATFOQKHINTPNCNTIMDNNIYVGGQCKRVNTFISSATTYKATCTGVINLV 60
 CC
 CC QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 CC Db 61 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 CC
 CC RESULT 3
 CC RNPL_RANCA STANDARD; PRT; 111 AA.
 CC ID RNPL_RANCA
 CC AC P14626;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Ribonuclease, liver (EC 3.1.27.5).
 CC OS Rana catesbeiana (Bull frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 CC NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RA Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
 RT liver.";

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MQNWATFQKHIIPTIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	585.5	96.8	133	1	RNPO_RANCA
2	451	74.5	111	1	LECS_RANJA
3	370	61.2	111	1	RNPL_RANJA
4	273.5	45.2	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANG3_MOUSE
6	149.5	24.7	145	1	ANGR_MOUSE
7	136.5	22.6	145	1	ANGI_MOUSE
8	131.5	21.7	124	1	RNP_BALAC
9	129.5	21.4	124	1	RNP_PIG
10	129.5	21.4	167	1	RNBR_BOVIN
11	127.5	21.1	119	1	RNP_IGUIG
12	124.5	20.6	151	1	RNBR_CAPCA
13	123.5	20.4	123	1	ANG2_BOVIN
14	123.5	20.4	141	1	RNBR_GIRCA
15	123.5	20.4	151	1	RNBR_AXIPR
16	123	20.3	146	1	ANGI_MIOTA
17	123	20.3	146	1	ANGI_SAIISC
18	120	19.8	146	1	ANGI_CERAE
19	120	19.8	147	1	ANGI_PONPY
20	119.5	19.8	143	1	RNBR_SHEEP
21	119	19.7	122	1	RNP_MACRU
22	118.5	19.6	123	1	ANGI_PIG
23	118.5	19.6	124	1	RNP_ANTAM
24	118	19.5	146	1	ANGI_AOTTR
25	117	19.3	146	1	ANGI_SAGOE
26	116.5	19.3	128	1	RNP_MYOCO
27	116.5	19.3	146	1	RNP_MOUSE
28	115	19.0	146	1	ANGI_MACMU
29	114.5	18.9	128	1	RNPB_CAVPO
30	114	18.8	148	1	ANGI_BOVIN
31	113.5	18.8	124	1	RNP_CAMDR
32	113.5	18.8	128	1	RNP_HORSE
33	113	18.7	147	1	ANGI_HUMAN

34	113	18.7	147	1	ANGI_PANTR	Q8wme8 pan troglod
35	112.5	18.6	119	1	RNS4_BOVIN	P15467 bos taurus
36	112.5	18.6	128	1	RNP_PROGU	P04059 proechimys
37	109.5	18.1	124	1	RNP_RANTA	P00666 rangifer ta
38	109.5	18.1	146	1	ANGI_PAPHA	Q8wn64 papio hamad
39	109.5	18.1	148	1	RNS4_MOUSE	Q91jhl mus musculus
40	109	18.0	125	1	ANGI_RABIT	P31347 oryctolagus
41	108.5	17.9	124	1	RNP_CAPCA	P00664 capreolus c
42	108.5	17.9	124	1	RNP_GIRCA	P00662 giraffa cam
43	108.5	17.9	130	1	RNP_CRILLO	P24717 cricetus
44	107.5	17.8	124	1	RNP_BUBBU	P00657 bubalus bub
45	107.5	17.8	148	1	RNP_PERLE	Q9wuv5 peromyscus

ALIGNMENTS

RESULT 1
RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q3PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
DE binding lectin) (SBL-C).
CN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Lu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity";
RL J. Biol. Chem. 273:6395-6401(1998).
RN [2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RT Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RT Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog);"
J. Mol. Biol. 283:231-244(1998).
CC !- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

Db 7 FORQMDTEHSPASSSNYNCLMMKAR-DWTSGRCKPLNTFIHPKSVVDVACHQENVTCK 65

QY 53 TGVINLVNLTTRFQNLCTRTSITPRP-CPYSSRTEITNYICVKENQY-PVHF 104

Db 66 NGRITNC-YKSNRLSITNCRTGASKYPCQYETSNLKQIIVACEGGQVFPVHF 118

RESULT 11

A43825

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S29834; A43825

R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.

Biochim. Biophys. Acta 1162, 177-186, 1993

A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme

A:Reference number: S29833; MUID:93192291; PMID:8448182

A:Accession: S29834

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-123 <BON>

A>Note: this sequence was submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

Query Match 19.6%; Score 118.5; DB 1; Length 123;

Best Local Similarity 39.5%; Pred. No. 9.2e-05;

Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

QY 34 CKRVNTEFISSATTVKAICTG---VINLVNLTTRFQNLCTRTSITPR-PCPYSSRTE 88

Db 39 CKVNTFHTGTRNDIKALCNKGEPYNNFRKSPFOITTCKHKGSGNRPPCGYRATAG 98

QY 89 TNYICVKENQYVHF 104

Db 99 FRTIIVACENGLPVHF 114

RESULT 12

NPRH

C:Species: Antilocapra americana (pronghorn)

A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw

C>Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000

C:Accession: A00813

R:Beintema, J.J.; Gaastra, W.; Munniksma, J.

J. Mol. Evol. 13, 305-316, 1979

A:Title: Evolution of pronghorn pancreatic ribonuclease: the mRNA sequence of mouse

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BEI>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12-41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.6%; Score 118.5; DB 1; Length 124;

Best Local Similarity 29.9%; Pred. No. 9.3e-05;

Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;

QY 5 ATFOQKHINTPI-----ICNTILDNNIYVGGCKRVNTFISSATTVKAICT- 53

Db 6 AKFERQHIDSNPSSVSSSNYNQNMKSR-NLTQGRCKPNTFVHESLADVQAVCSQKNVA 64

QY 54 ---GVINLVNLTTRFQNLCTRTSITPRP-CPYSSRTEITNYICVKCE-NQY-PVHF 104

Db 65 CKNGTNC-YOYSTMSITDCRETSGSKYPNCAYKTTQAKKHIIIVACEGNPVPVHY 120

RESULT 13

NRCU

C:Species: Myocastor coypus (nutria, coypu)

C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1998 #text_change 31-Mar-2000

C:Accession: A00822

R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.

Biochim. Biophys. Acta 453, 400-409, 1976

A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic

A:Reference number: A90612; MUID:77065676; PMID:999896

A:Accession: A00822

A:Molecule type: protein

A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12-41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.3%; Score 116.5; DB 1; Length 128;

Best Local Similarity 30.8%; Pred. No. 0.00015;

Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 7 FQQRKH-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 60

Db 8 FERQHMDSRGSPSTNPNYCNEMKSR-NMTQGRCKPNTFVHEPLADVQAVC---FQKRV 63

QY 61 L-----STTRFQNLCTRTSITPRP-CPYSSRTEITNYICVKCE-NQY-PVHF 104

Db 64 LCKNGTNCYQSNMHTDCRVTSNSDPNCSYTSQEEKSIIVACEGNPVPVHF 120

RESULT 14

NRMS

C:Species: Mus musculus (house mouse)

C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: A34090; S22598; A00830

R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.

Mol. Biol. Evol. 7, 29-44, 1990

A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse

A:Reference number: A34090; MUID:90136034; PMID:2299980

A:Accession: A34090

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <SCH>

A:Cross-references: GB:M27814; NID:G200762; PIDN:AAA40060.1; PID:G200763

R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.

Nucleic Acids Res. 19, 6935-6941, 1991

A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific

A:Reference number: S22598; MUID:92107684; PMID:1840677

A:Accession: S22598

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <SAM>

A:Cross-references: EMBL:X61013; NID:G53981; PIDN:CAA42697.1; PID:G53982

R:Lenstra, J.A.; Beintema, J.J.

Eur. J. Biochem. 98, 399-408, 1979

A:Title: The amino acid sequence of mouse pancreatic ribonuclease.

A:Reference number: A00830; MUID:80024269; PMID:556267

A:Accession: A00830

A:Molecule type: protein

A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:1-25/Domain: signal sequence #status predicted <Sig>

F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>

F:37,66,144/Active site: His, Lys, His #status predicted

F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted

F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.3%; Score 116.5; DB 1; Length 149;

Best Local Similarity 29.9%; Pred. No. 0.00018;

Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;

Query Match 21.4%; Score 129.5; DB 2; Length 167;
Best Local Similarity 30.6%; Pred. No. 1e-05;
Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

QY	5	AATFOOKHI-----INTPIICNTILDNNIIVYGQQCKVNTFISSATTVAICTGVINL	58
DB	32	AKFRQHMDGSGSSSNPNYCMMKKR-RMTHGRCKPWNFVBHSLDDVKAVCS---QK	87
		: :: :	:
QY	59	NVL-----SSTRFQLTCTRTISITPRP-CFYSSRTETNYICVKE-NQY-PVHFA	105
DB	88	NITCKNGHPNCVQSXSMTSIDCRTGTSSKYPCAYKTSQKQKIYTACEGNYPVVHF	147
		:: :	:: :: :
QY	106	G 106	
DB	148	G 148	

RESULT 9

S41lll	pancreatic ribonuclease - common iguana
C;Species:	Iguana iguana (common iguana)
C;Date:	19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession:	S41lll
R;Zhao, W.; Beintema, J.J.;; Hofsteenge, J.	Eur. J. Biochem. 219, 641-646, 1994
A;Title:	The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number:	S41lll; PMID:94139745; PMID:8307028
A;Accession:	S41lll
A>Status:	preliminary
A:Molecule type:	protein
A;Residues:	1-119 <ZHA>
C;Superfamily:	pancreatic ribonuclease

Query Match	21.1%; Score 127.5; DB 2; Length 119;
Best Local Similarity	29.6%; Pred. No. 1.e-05;
Matches	34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

QY	2	QNWATFOOHH-----INTPIICNTILDNNIIVYGQQCKRVNFTFISSATTVAICA--	52
DB	1	QDWSSFONKHIDYPETSASNPAYCDLMQRRLNLPTKCCKTRNTFFVASPSIQVCGS	59
		:: :	: :: :
QY	53	--TGVINLVLTSTTFQNTCTRTSIT-PRCPYSRSRTETNYICVKCENQYEVHF	104
DB	60	GGTHVEDNLYDSNESFDLTDCNQVGTPAPSCCKXNGTPTGKRIRACENNQPVFH	114
		:: :	: :: :

RESULT 10
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N;Alternate names: RNase I; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaastera, W.; Wellington, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; PMID:78190621; PMID:658039
A;Accession: A00833
A:Molecule type: protein
A;Residues: 1-122 <CAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match	19.7%; Score 119; DB 1; Length 122;
Best Local Similarity	29.8%; Pred. No. 8.2e-05;
Matches	34; Conservative 17; Mismatches 45; Indels 18; Gaps 6;

QY	7	FQOHKI-----INTPIICNTILDNNIIVYGQQCKRVNFTFISSATTVAICA-	52
		:: :	: :: :

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 10.072 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MQNWATFQOKHIINTPICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 2833366

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

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Database : PIR_78:*
1:  pir1:*
2:  pir2:*
3:  pir3:*
4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	582.5	96.3	111	1	2	A27121	ribonuclease-relat
2	451	74.5	111	1	2	JX0120	ribonuclease-relat
3	370	61.2	111	2	2	JX0085	pancreatic ribonuc
4	270.5	44.7	104	2	2	A39035	ribonuclease-relat
5	136.5	22.6	145	1	1	A39332	angiolegenin precurs
6	131.5	21.7	124	1	1	NRNWK	pancreatic ribonuc
7	129.5	21.4	124	1	1	NRPG	pancreatic ribonuc
8	129.5	21.4	167	2	2	S20066	pancreatic-type ri
9	127.5	21.1	119	2	2	S41111	pancreatic ribonuc
10	119	19.7	122	1	1	NRXGR	pancreatic ribonuc
11	118.5	19.6	123	1	1	A43825	angiolegenin - pig
12	118.5	19.6	124	1	1	NRBRH	pancreatic ribonuc
13	116.5	19.3	128	1	1	NRPU	pancreatic ribonuc
14	116.5	19.3	149	1	1	NRMS	pancreatic ribonuc
15	114.5	18.9	128	1	1	NRGPB	pancreatic ribonuc
16	114	18.8	125	1	1	A32474	angiolegenin [valida
17	113.5	18.8	124	1	1	NRCCM	pancreatic ribonuc
18	113.5	18.8	124	1	1	NRCCM	pancreatic ribonuc
19	113.5	18.8	124	1	1	NRCCB	pancreatic ribonuc
20	113.5	18.8	128	1	1	NRHO	pancreatic ribonuc
21	113	18.7	147	1	1	NRHUAG	angiolegenin precurs
22	112.5	18.6	128	1	1	NRXS	pancreatic ribonuc
23	110.5	18.3	124	2	2	S08549	ribonuclease - dom
24	109.5	18.1	124	1	1	NRDEN	pancreatic ribonuc
25	109	18.0	125	1	1	A43825	angiolegenin - rabbi
26	108.5	17.9	124	1	1	NRGFG	pancreatic ribonuc
27	108.5	17.9	124	1	1	NRDEO	pancreatic ribonuc
28	108.5	17.9	130	2	2	S22808	pancreatic ribonuc
29	107.5	17.8	124	1	1	NRWB	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
Ribonuclease-related sialic acid-binding lectin - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change
C/Accession: A27121
R/Tittari, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, Biochemistry 26, 2189-2194, 1987
A;Title: Amino acid sequence of sialic acid-binding lectin
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match	96.3%	Score 582.5;	DB 2;	Length 111;
Best Local Similarity	96.4%;	Pred. No. 9.5e-51;		
Matches 107;	Conservative 3;	Mismatches 0;	Indels 1;	Gaps 1;

Qy	2	QNWATFQKHINTPII-CNTILDNNIYIVGGCKRVNTEFIISATTVKAICTGVINLNV	60
	:	: :	
Db	1	ENWATFQKHINTPIINCNTIMDNNIYIVGGCKRVNTEFIISATTVKAICTGVINLNV	60
	:	: :	
Qy	61	LSSTRFQLNCTRTSITPRPCPYSSSTETNYICVKENQYPVHFAGIGRCP	111
	:	: :	
Db	61	LSSTRFQLNCTRTSITPRPCPYSSSTETNYICVKENQYPVHFAGIGRCP	111
	:	: :	

RESULT 2

JX0120
 ribonuclease-related sialic acid-binding lectin - Japanese frog
 C;Species: Rana japonica (Japanese frog)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: JX0120
 R;Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takai
 J. Biochem. 108, 139-149, 1990
 A;Title: Amino acid sequence of a lectin from Japanese frog (*Rana japonica*) eggs.
 A;Reference number: JX0120; MUID:91035319; PMID:2229005
 A;Accession: JX0120
 A;Molecule type: protein
 A;Residues: 1-111 <KAM>
 A;Experimental source: egg
 C;Superfamily: pancreatic ribonuclease
 C;Keywords: lectin; pyrrolidone acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 74.5%; Score 451; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1e-37;
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;


```

; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
; OTHER INFORMATION: Met57Leu substitutions (recombinant RaCOR1
; OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match          98.2%; Score 594; DB 10; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.3e-59;
Matches 109; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 60

Qy 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 13
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
; OTHER INFORMATION: (recombinant RaCOR1 Q1S)
US-09-948-391A-24

Query Match          97.7%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 62
Db 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61

Qy 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 14
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match          97.7%; Score 591; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.9e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 62
Db 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNLV 61

Qy 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 110

RESULT 15
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT

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Db 1 QNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
Qy 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 9
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RacOR1 QIS)
US-09-948-391A-26

Query Match 98.5%; Score 596; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 7.9e-60;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
Db 1 MSNWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 10
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: (recombinant Met(-1) RacOR1)
US-09-948-391A-17

Query Match 98.3%; Score 595; DB 10; Length 111;
Best Local Similarity 97.3%; Pred. No. 1e-59;
Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
Db 1 MOWWATFOQKHINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 12
US-09-948-391A-19
; Sequence 19, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
```

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; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; US-09-961-400-17

Query Match
Best Local Similarity 99.3%; Score 601; DB 10; Length 111;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MONWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60
Db 1 MONWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 6
US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; US-09-961-400-19

Query Match
Best Local Similarity 99.2%; Score 600; DB 10; Length 110;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 61
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60

QY 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 7
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; US-09-961-400-15

Query Match
Best Local Similarity 98.2%; Score 596; DB 10; Length 110;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 61
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60

QY 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

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; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
; US-09-948-391A-15

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Query Match
Best Local Similarity 98.5%; Score 596; DB 10; Length 110;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 61
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

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RESULT 8
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
; US-09-961-400-15

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Query Match
Best Local Similarity 98.5%; Score 596; DB 10; Length 110;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 61
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 60

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Db 1 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-09-961-400-21
; Sequence 21, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-21

Query Match 100.0%; Score 605; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 1 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu- (His)6)
US-09-948-391A-22

Query Match 100.0%; Score 605; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
Db 7 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 4
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 100.0%; Score 605; DB 10; Length 117;
Best Local Similarity 100.0%; Pred. No. 8e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 7 MONWATFOOKHILNTPILCNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 5
US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:29:40 ; Search time 35.6155 Seconds
(without alignments)
865.070 Million cell updates/sec

Title: US-09-961-400-21
Perfect score: 605
Sequence: 1 MNWATFQKHIIPTICN.....ICVKCENQYVHFAGIGRCP 111

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Total number of hits satisfying chosen parameters: 1140673

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	605	100.0	111	10	US-09-948-391A-21
2	605	100.0	111	10	US-09-961-400-21
3	605	100.0	117	10	US-09-948-391A-22
4	605	100.0	117	10	US-09-961-400-22
5	601	99.3	111	10	US-09-961-400-17
6	600	99.2	110	10	US-09-961-400-19
7	596	98.5	110	10	US-09-948-391A-15
8	596	98.5	110	10	US-09-961-400-15
9	596	98.5	111	10	US-09-948-391A-26
10	596	98.5	111	10	US-09-961-400-26
11	595	98.3	111	10	US-09-948-391A-17
12	594	98.2	110	10	US-09-948-391A-19
13	591	97.7	110	10	US-09-948-391A-24
14	591	97.7	110	10	US-09-961-400-24
15	284.5	47.0	111	10	US-09-961-400-9

15	282.5	45.7	105	10	US-09-948-391A-6	Sequence 6, Appli
17	282.5	46.7	105	10	US-09-961-400-6	Sequence 6, Appli
18	281.5	46.5	105	10	US-09-961-400-8	Sequence 8, Appli
19	278.5	46.0	105	14	US-10-153-882-2	Sequence 2, Appli
20	277.5	45.9	104	10	US-09-961-400-2	Sequence 2, Appli
21	277.5	45.9	105	10	US-09-948-391A-13	Sequence 13, Appli
22	277.5	45.9	105	10	US-09-961-400-13	Sequence 13, Appli
23	277.5	45.9	127	10	US-09-948-391A-28	Sequence 28, Appli
24	277.5	45.9	127	10	US-09-961-400-28	Sequence 28, Appli
25	276.5	45.7	104	10	US-09-948-391A-2	Sequence 2, Appli
26	276.5	45.7	104	10	US-09-948-391A-4	Sequence 4, Appli
27	276.5	45.7	104	10	US-09-961-400-4	Sequence 4, Appli
28	272.5	45.0	104	10	US-09-948-391A-11	Sequence 11, Appli
29	272.5	45.0	104	10	US-09-961-400-11	Sequence 11, Appli
30	272.5	45.0	105	10	US-09-948-391A-8	Sequence 8, Appli
31	272.5	45.0	111	10	US-09-948-391A-9	Sequence 9, Appli
32	268.5	44.4	104	9	US-09-986-119-1	Sequence 1, Appli
33	268.5	44.4	104	10	US-09-918-887-1	Sequence 1, Appli
34	265.5	43.9	104	12	US-10-461-713-53	Sequence 53, Appli
35	202	33.4	83	9	US-09-986-119-3	Sequence 3, Appli
36	202	33.4	83	10	US-09-918-887-3	Sequence 3, Appli
37	161	26.6	169	13	US-10-016-447-2	Sequence 2, Appli
38	131.5	21.7	124	12	US-10-037-417-103	Sequence 103, App
39	127.5	21.1	119	12	US-10-016-248-89	Sequence 89, Appl
40	127.5	21.1	119	15	US-10-074-978A-139	Sequence 139, App
41	118	19.5	99	15	US-10-074-978A-141	Sequence 141, App
42	117	19.3	147	9	US-09-731-872-254	Sequence 254, App
43	117	19.3	147	10	US-09-876-997-254	Sequence 254, App
44	114	18.8	123	12	US-10-461-713-58	Sequence 58, Appl
45	114	18.8	124	13	US-10-016-447-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-948-391A-21
; Sequence 21, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbelana ribonuclease with Met at position 1,
; OTHER INFORMATION: Met23Leu and Met58Leu substitutions (recombinant
; OTHER INFORMATION: Met(-1) RacOR1 Met22Leu Met57Leu)
US-09-948-391A-21

Query Match 100.0%; Score 605; DB 10; Length 111;
Best Local Similarity 100.0%; Pred. No. 7.5e-61;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MNWATFQKHIIPTICNTILDNIYIVGGQCKRVNTFISSATTVKAICTGVINLV 60

APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-59

Query Match 45.2%; Score 273.5; DB 3; Length 251;
Best Local Similarity 48.2%; Pred. No. 8.2e-24;
Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

OY 1 MQNWATFQCKHINT-PIICNTILDNNIYVGGQCKRVNTEIISSTATTVKAICTGVI-NL 58
DB 147 MSDWLTFFQCKHINTTRDVEDCDNIMSTNLF---HCKDKNTFIYSRPEPVPKAIKGIASK 202

OY 59 NVLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCNQYVPVHPAGIGRC 110
DB 203 NVLTTFSEFVLSDC--NVTSRCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 251

Search completed: May 7, 2004, 21:40:46
Job time : 12.8756 secs

; MOLECULE TYPE: protein
US-09-095-429-1

Query Match 45.2%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59
Db 1 QDWLTFQKKHITNTRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 57 VLTTSFYLSDC---NVTSPCKYKLLKSTNKFVCVTCEQAPVHFVGVGSC 104

RESULT 13
US-08-875-811-32

; Sequence 32, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-32

Query Match 45.2%; Score 273.5; DB 3; Length 112;
Best Local Similarity 48.2%; Pred. No. 3.1e-24;
Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

QY 1 MNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NL 58
Db 8 MSWLTFOKKHITNTRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63

QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110

Db 64 NVLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVTCEQAPVHFVGVGSC 112

RESULT 14

US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-63

Query Match 45.2%; Score 273.5; DB 3; Length 129;
Best Local Similarity 48.6%; Pred. No. 3.7e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 59
Db 26 QDWLTFQKKHITNTRDVCDCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 81

QY 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 82 VLTTSFYLSDC---NVTSPCKYKLLKSTNKFVCVTCEQAPVHFVGVGSC 129

RESULT 15

US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis

RESULT 11
 US-08-626-288-1
 ; Sequence 1, Application US/06626288
 ; Patent No. 6649392
 ; GENERAL INFORMATION:
 ; APPLICANT: Youle, Richard
 ; APPLICANT: Vasandani, Veena
 ; APPLICANT: Wu, Yon-Neng
 ; APPLICANT: Boix, Ester
 ; APPLICANT: Ardelt, Wojciech
 ; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
 ; TITLE OF INVENTION: Allows Production by Recombinant Methods
 ; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew
 ; STREET: One Market Plaza, Steuart Street Tower
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94105-1492
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/626,288
 ; FILING DATE: No. 6649392 yet assigned
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:

```

RESULT 12
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649393
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Wu, Yon-Neng
; APPLICANT: Boix, Ester
; APPLICANT: Ardelet, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; TITLE OF INVENTION: Allows Production by Recombinant Methods
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,429
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear

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APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 45.5%; Score 275.5; DB 3; Length 358;
Best Local Similarity 48.2%; Pred. No. 7.5e-24;
Matches 54; Conservative 17; Mismatches 32; Indels 9; Gaps 4;
Qy 1 MONWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NL 58
Db 1 MEDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56
Qy 59 NVLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
Db 57 NVLTSEFYLSDC---NVTSRCKYKLKSTNKFVCVTENQAPVHFVGVGSC 105

RESULT 7
US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 45.2%; Score 273.5; DB 3; Length 104;

Best Local Similarity 48.6%; Pred. No. 2.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 1 QDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
Qy 60 VLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
Db 57 VLTTSEFYLSDC---NVTSRCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 8
US-09-394-268-2
Sequence 2, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
OTHER INFORMATION: position 72
US-09-394-268-2

Query Match 45.2%; Score 273.5; DB 3; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.8e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
Db 1 QDWLTFOKKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
Qy 60 VLSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
Db 57 VLTTSEFYLSDC---NVTSRCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

RESULT 9
US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.2%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Qy 2 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..111
OTHER INFORMATION: /note= "Frog Lectin from Rana
US-08-891-848-12
Query Match 96.3%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
QY 2 QNWATFQOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
Db 1 ENWATFQOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
RESULT 2
US-08-875-811-8
Sequence 8, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..111

OTHER INFORMATION: /note= "Frog Lectin from Rana
US-08-875-811-8
Query Match 96.3%; Score 582.5; DB 3; Length 111;
Best Local Similarity 96.4%; Pred. No. 5.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
QY 2 QNWATFQOKHIINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
Db 1 ENWATFQOKHIINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINLV 60
QY 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
RESULT 3
US-08-467-955-2
Sequence 2, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D. Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:28:45 ; Search time 12.8756 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-21

Perfect score: 605

Sequence: 1 MQNWTQQKHINTPICN.....ICVKENQYVHFAGIGRCP 111

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	582.5	96.3	111	3	US-08-875-811-8
3	280.5	46.4	104	1	US-08-467-955-2
4	275.5	45.5	105	3	US-08-875-811-39
5	275.5	45.5	355	3	US-08-875-811-41
6	275.5	45.5	358	3	US-08-875-811-51
7	273.5	45.2	104	3	US-09-394-268-1
8	273.5	45.2	104	3	US-09-394-268-2
9	273.5	45.2	104	4	US-09-687-748-1
10	273.5	45.2	104	4	US-09-687-748-2
11	273.5	45.2	104	4	US-09-626-288-1
12	273.5	45.2	104	4	US-09-095-429-1
13	273.5	45.2	112	3	US-08-875-811-32
14	273.5	45.2	129	3	US-08-875-811-63
15	273.5	45.2	251	3	US-08-875-811-59
16	273.5	45.2	254	3	US-08-875-811-61
17	273.5	45.2	355	3	US-08-875-811-49
18	273.5	45.2	355	3	US-08-875-811-57
19	273.5	45.2	355	3	US-08-875-811-64
20	273.5	45.2	366	3	US-08-875-811-55
21	273.5	45.2	379	3	US-08-875-811-43
22	270.5	44.7	104	1	US-08-283-971-1
23	270.5	44.7	104	1	US-07-921-619-1
24	270.5	44.7	104	1	US-08-467-955-1
25	270.5	44.7	104	1	US-08-891-848-13
26	270.5	44.7	104	4	US-08-626-288-2
27	270.5	44.7	104	4	US-09-095-429-2

28 268.5 44.4 104 3 US-08-875-811-1 Sequence 1, Appli
29 268.5 44.4 104 4 US-09-071-672-1 Sequence 1, Appli
30 268.5 44.4 104 4 US-09-986-119-1 Sequence 1, Appli
31 268.5 44.4 105 3 US-08-875-811-26 Sequence 26, Appli
32 268.5 44.4 106 3 US-08-875-811-28 Sequence 28, Appli
33 268.5 44.4 107 3 US-08-875-811-30 Sequence 30, Appli
34 267.5 44.2 105 3 US-08-875-811-30 Sequence 24, Appli
35 264.5 43.7 358 3 US-08-875-811-45 Sequence 45, Appli
36 264.5 43.7 365 3 US-08-875-811-53 Sequence 53, Appli
37 246.5 40.7 107 3 US-08-875-811-20 Sequence 20, Appli
38 235.5 38.9 111 3 US-08-875-811-22 Sequence 22, Appli
39 232 38.3 114 3 US-09-223-118-3 Sequence 3, Appli
40 228.5 37.8 360 3 US-08-875-811-47 Sequence 47, Appli
41 223 36.9 114 3 US-09-223-118-2 Sequence 2, Appli
42 222 36.7 114 3 US-09-223-118-1 Sequence 1, Appli
43 221 36.5 114 3 US-09-223-118-4 Sequence 4, Appli
44 202 33.4 83 3 US-08-875-811-2 Sequence 2, Appli
45 202 33.4 83 4 US-09-071-672-3 Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Neeton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION NUMBER: US 08/014,082
; APPLICATION DATA:
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

```

OS Rana pipiens.
OS Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /note= "Met not found in wild type RaPLR1"
XX Misc-difference 2 /note= "Wild type Gln replaced with Ser"
XX
XX
XX WO9950398-A2.
XX
XX PD
XX 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US006641.
XX
XX PR 27-MAR-1998; 98US-0079751P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Rybak SM, Newton DL;
XX
XX DR WPI; 1999-610847/52.
XX DR N-PSDB; AAZ08129.
XX
XX PR New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX PS Claim 34; Page 61; 71pp; English.
XX
XX CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
XX protein with Met at position 1 and Gln2Ser. Carboxy terminal end of
XX recombinant RaPLR1 has a covalently bound ligand binding moiety, which
XX can be a LL2 antibody directed against CD22 on cancerous B cells or human
XX chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.
XX Recombinant ribonucleases can be expressed in bacteria without an N-
XX terminal methionine due to the presence of a signal peptide that is
XX cleaved by bacteria. The soluble expression of ribonuclease allows the
XX proteins to be fused in-frame with ligand binding moieties to form
XX cytotoxic fusion proteins. They can be used for treatment of cancer and
XX autoimmune diseases
XX
XX SQ Sequence 105 AA;
XX
XX Query Match 45.9%; Score 277.5; DB 2; Length 105;
XX Best Local Similarity 48.2%; Pred. No. 1.9e-23;
XX Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;
XX
XX QY 1 MQNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NL 58
XX Db 1 MSDWLTFOKKHLNTRDVCNNIMSTNLF---HCKDKNTFYISRPVPVKAICKGIASK 56
XX
XX QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
XX Db 57 NVLTSEFVLSDC---NVTSPCKYKLKSKSTNTFCVTCENQAPVHFVGVGHC 105
XX
XX RESULT 15
XX AAY28879
XX ID AAY28879 standard; protein; 127 AA.
XX
XX AC AAY28879;
XX
XX DT 25-JAN-2000 (first entry)
XX
XX DE Rana pipiens Clone 5a1b ribonuclease.
XX
XX KW Rana pipiens ribonuclease Clone 5a1b; RaPLR1; covalently bound; RNase;
XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
XX Kaposi's Sarcoma; human chorionic gonadotropin; hCG; cancer;
XX recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
XX autoimmune disease.
XX
XX OS Rana pipiens.

```

```

XX Key Location/Qualifiers
XX Peptide 1. .23
XX /label= Signal_peptide
XX /note= "Putative"
XX
XX Protein 24. .127
XX /label= Rana_pipiens_Clone_5a1b_ribonuclease
XX
XX PN WO9950398-A2.
XX
XX XX 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US006641.
XX
XX PR 27-MAR-1998; 98US-0079751P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Rybak SM, Newton DL;
XX
XX DR WPI; 1999-610847/52.
XX DR N-PSDB; AAZ08136.
XX
XX PR New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX PS Disclosure; Page 69; 71pp; English.
XX
XX CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaPLR1).
XX It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
XX library. It exhibits differences with Onconase (RTM) at amino acid
XX residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a
XX covalently bound ligand binding moiety, which can be a LL2 antibody
XX directed against CD22 on cancerous B cells or human chorionic
XX gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
XX ribonucleases can be expressed in bacteria without an N-terminal
XX methionine due to the presence of a signal peptide that is cleaved by
XX bacteria. The soluble expression of ribonuclease allows the proteins to
XX be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX proteins. They can be used for treatment of cancer and autoimmune
XX diseases
XX
XX SQ Sequence 127 AA;
XX
XX Query Match 45.9%; Score 277.5; DB 2; Length 127;
XX Best Local Similarity 48.6%; Pred. No. 2.4e-23;
XX Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
XX
XX QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NLN 59
XX Db 24 QDWLTFOKKHLNTRDVCNNIMSTNLF---HCKDKNTFYISRPVPVKAICKGIASKN 79
XX
XX QY 60 VLSSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
XX Db 80 VLTITSEFVLSDC---NVTSPCKYKLKSKSTNTFCVTCENQAPVHFVGVGHC 127
XX
XX Search completed: May 7, 2004, 21:38:29
XX Job time : 47.3489 secs

```

AC AAY39400;
 XX
 DT 01-DEC-1999 (first entry)
 DE Recombinant frog Onconase.
 XX
 KW Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
 XX
 OS Rana pipiens.
 XX
 PN WO9946389-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 11-MAR-1999; 99WO-US004252.
 XX
 PR 11-MAR-1998; 98US-0077557P.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 PI Goldenberg DM, Hansen H, Leung S;
 XX
 DR WPI: 1999-551416/46.
 DR N-PSDB; AAZ19767.
 XX
 PT A new recombinant Onconase used to treat, e.g. colon cancer.
 PS Example 1; Fig 1; 42pp; English.
 XX
 CC This sequence represents recombinant frog Onconase. Onconase has
 CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR
 CC (using primers AAZ19768-Z19769) of two synthetic DNAs whose sequences
 CC encoded most of the N-terminal or the C-terminal amino acids of mature
 CC Onconase. The two PCR products generated encoded either the N-terminal 54
 CC amino acids (minus the initial methionine) or the C-terminal 51 amino
 CC acids, and were ligated in frame at a NruI site. The cDNA was then
 CC subcloned into a vector e.g., pBluescript, where the ATG initiation codon
 CC was ligated to the cDNA. After expression in E. coli, the recombinant
 CC protein was purified. The initial N-formyl methionine was cleaved off and
 CC the new N-terminal glutamate residue cyclised to form an N-terminal
 CC pyroglutamate. The pyroglutamate residue forms part of the phosphate
 CC binding pocket of Onconase and is essential for both ribonuclease and anti-
 CC -tumour activity. Onconase is a 12 kD ribonuclease which causes cell
 CC death as a result of potent inhibition of protein synthesis by a
 CC mechanism involving inactivation of cellular RNA. It is not inhibited by
 CC mammalian placental ribonuclease inhibitor, which may explain its
 CC enhanced cytotoxicity relative to mammalian enzymes. It has anti-tumour
 CC activity against a variety of solid tumours e.g. colon or pancreatic
 CC cancers, and can be used alone or in combination with other anti-cancer
 CC agents such as tamoxifen. When used as an anti-tumour agent, Onconase can
 CC be conjugated to a marker which targets it to a specific cell type
 XX
 SQ Sequence 105 AA;
 Query Match 46.0%; Score 278.5; DB 2; Length 105;
 Best Local Similarity 49.4%; Pred. No. 1.5e-23;
 Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
 QY 1 MQNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATVKAICTGVI-NLN 58
 Db 1 MQWLTFOQKHINTKDVCDDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSK 56
 QY 59 NVLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 Db 57 NVLTSEFYLSDC--NVTSRPCKYKLKSTNFKVCTCENQAPVHFVGVGSC 105
 RESULT 13
 AAY28865
 ID AAY28865 standard; protein; 104 AA.
 XX
 AC AAY28865;
 XX

DT 25-JAN-2000 (first entry)
 XX
 DE Rana pipiens liver ribonuclease (RaPLR1).
 XX
 KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
 KW ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX
 OS Rana pipiens.
 XX
 PN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI: 1999-610847/52.
 DR N-PSDB; AAZ08124.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.
 PS Claim 1; Page 55; 71pp; English.
 XX
 CC The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
 CC Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
 CC moiety, which can be a LL2 antibody directed against CD22 on cancerous B
 CC cells or human chorionic gonadotrophin (hCG) effective against Kaposi's
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 CC without an N-terminal methionine due to the presence of a signal peptide
 CC that is cleaved by bacteria. The soluble expression of ribonuclease
 CC allows the proteins to be fused in-frame with ligand binding moieties to
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 CC and autoimmune diseases
 XX
 SQ Sequence 104 AA;
 Query Match 45.9%; Score 277.5; DB 2; Length 104;
 Best Local Similarity 48.6%; Pred. No. 1.9e-23;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
 QY 2 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATVKAICTGVI-NLN 59
 Db 1 QDWLTFOQKHINTRDVCDDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 56
 QY 60 VLSTTRFQNLNCTRTSITPRCPYSSRTETNYICVKCENQYVHFAGIGRC 110
 Db 57 VLTTSEFYLSDC--NVTSRPCKYKLKSTNFKVCTCENQAPVHFVGVGHC 104
 RESULT 14
 AAY28871
 ID AAY28871 standard; protein; 105 AA.
 XX
 AC AAY28871;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaPLR1 Gln1Ser amino acid sequence.
 XX
 KW Recombinant Met (-1) Rana pipiens ribonuclease Gln1Ser; RaPLR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease; RNase.
 XX

AA2886	AA28866 standard; protein; 104 AA.
XX	AC AAY28866;
XX	25-JAN-2000 (first entry)
XX	Recombinant RapLr1 Met23Leu amino acid sequence.
DE	Recombinant Rana pipiens ribonuclease; RapLr1 Met23Leu; covalently bound;
XX	LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
XX	Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW	recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW	autoimmune disease.
XX	
OS	Rana pipiens.
OS	Synthetic.
XX	
XX	Key Location/Qualifiers
FF	Misc-difference 23
FT	/note= "Wild type Met replaced with Leu"
FT	
XX	WO9950398-A2.
PN	07-OCT-1999.
XX	26-MAR-1999; 99WO-US006641.
XX	27-MAR-1998; 98US-0079751P.
PR	(USSH) US DEPT HEALTH & HUMAN SERVICES.
XX	
XX	Rybak SM, Newton DL;
PI	WPI: 1999-610847/52.
DR	N-PSDB; AA208125.
DR	
XX	
XX	New recombinant ribonucleases, used for killing target cells, e.g. for
PT	treating cancers, viral infections or autoimmune diseases.
PT	
XX	Claim 34; Page 56; 71pp; English.
PS	
PS	The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)
XX	protein with Met23Leu. Carboxy terminal end of recombinant RapLr1 has a
CC	covalently bound ligand binding moiety, which can be a LL2 antibody
CC	directed against CD22 on cancerous B cells or human chorionic
CC	gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC	ribonucleases can be expressed in bacteria without an N-terminal
CC	methionine due to the presence of a signal peptide that is cleaved by
CC	bacteria. The soluble expression of ribonuclease allows the proteins to
CC	be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC	proteins. They can be used for treatment of cancer and autoimmune
CC	diseases
XX	
XX	Sequence 104 AA;
XX	
XX	Query Match 46.2%; Score 279.5; DB 2; Length 104;
XX	Best Local Similarity 49.5%; Pred. No. 1.1e-23;
XX	Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4
QY	2 QNWATFQOQHIINT-PIICNTILDNNIYIVGGCKRVNTFTIISATTVKAICTGVI-NLN 59
DB	1 QDWLTFQKHLTWTRDVCNNILSTNLF---HCKDKNTFIYSRPEVPYKAICKGIIASKN 56
QY	60 VLSTTRPQLNCTRTSTIPRCPYSGRTETNYICVKCENQYVHFAGIGRC 110
DB	57 VLRTSFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
XX	
XX	RESULT 12
XX	AA239400
XX	ID AAY39400 standard; protein; 105 AA.
XX	

CC (Rana catesbeiana) lectin used to describe the method of the invention
 XX
 SQ Sequence 111 AA;
 Query Match 96.3%; Score 582.5; DB 2; Length 111;
 Best Local Similarity 96.4%; Pred. No. 6.3e-58;
 Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;
 QY 2 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 ENWATFOQKHINTPIINCNIYMDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 61 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGICRCP 111
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 61 LSTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGICRCP 111
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 RESULT 8
 AAY28869
 ID AAY28869 standard; protein; 105 AA.
 XX
 AC AAY28869;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaPLR1 Met23Leu- (His)6 protein.
 XX
 KW Recombinant Met (-1) Rana pipiens ribonuclease Met23Leu- (His)6; RaPLR1;
 CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; frog; autoimmune disease.
 XX
 OS Rana pipiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 24 /note= "Wild type Met replaced with Leu"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08127.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 4; Page 59; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana pipiens ribonuclease protein
 (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
 CC Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
 CC binding moiety, which can be a LL2 antibody directed against CD22 on
 CC cancerous B cells or human chorionic gonadotrophin (hCG) effective
 CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
 CC expressed in bacteria without an N-terminal methionine due to the
 CC presence of a signal peptide that is cleaved by bacteria. The soluble
 CC expression of ribonuclease allows the proteins to be fused in-frame with

CC ligand binding moieties to form cytotoxic fusion proteins. They can be
 CC used for treatment of cancer and autoimmune diseases
 XX
 SQ Sequence 105 AA;
 Query Match 47.0%; Score 284.5; DB 2; Length 105;
 Best Local Similarity 50.0%; Pred. No. 3.1e-24;
 Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 1 MONWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGYI-NL 58
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 1 MODMLTFQKGLNTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASK 56
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 QY 59 NVLSITRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGICR 110
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 Db 57 NVLTTFEFLSDC----NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVC 105
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 RESULT 9
 AAY28867
 ID AAY28867 standard; protein; 105 AA.
 XX
 AC AAY28867;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaPLR1.
 XX
 KW Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
 covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.
 XX
 OS Rana pipiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 XX
 FN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Rybak SM, Newton DL;
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08126.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 treating cancers, viral infections or autoimmune diseases.
 XX
 PS Claim 34; Page 57; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1. Carboxy terminal end of recombinant
 CC RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX

CC autoimmune diseases

XX Sequence 111 AA;

SQ Sequence 111 AA;

Query Match 98.5%; Score 596; DB 2; Length 111;

Best Local Similarity 97.3%; Pred. No. 1.9e-59;

Matches 108; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNWATFQOKHIINTPIICNTILDNNIYIVGGCKRVNTFIISATTVKAICTGVINLV 60

Db 1 MSNWATFQOKHIINTPIICNTIMDNNIYIVGGCKRVNTFIISATTVKAICTGVINNV 60

QY 61 LSTRFQNLCTCTRTSIPTPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

Db 61 LSTRFQNLCTCTRTSIPTPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 6

AAV28877

ID AAY28877 standard; protein; 110 AA.

XX AAY28877;

AC AAY28877;

XX 25-JAN-2000 (first entry)

XX Recombinant RaCOR1 Gln1Ser amino acid sequence.

XX Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;

KW covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;

KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;

KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

KW cancer; autoimmune disease.

XX Rana catesbeiana.

OS Synthetic.

XX Key

XX Location/Qualifiers

XX Misc-difference 1

XX /note= "Wild type Gln replaced with Ser"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-P5DB; AAZ08134.

XX New recombinant ribonucleases, used for killing target cells, e.g. for

XX treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 67; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana oocyte

XX ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of

XX recombinant RaCOR1 has a covalently bound ligand binding moiety, which

XX can be a L12 antibody directed against CD22 on cancerous B cells or human

XX chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

XX Recombinant ribonucleases can be expressed in bacteria without an N-

XX terminal methionine due to the presence of a signal peptide that is

XX cleaved by bacteria. The soluble expression of ribonuclease allows the

XX proteins to be fused in-frame with ligand binding moieties to form

XX cytotoxic fusion proteins. They can be used for treatment of cancer and

XX autoimmune diseases

XX Sequence 110 AA;

SQ

Query Match

Best Local Similarity

Matches 107; Conservative

QY 3 NWATFQOKHIINTPIICNTILDNNIYIVGGCKRVNTFIISATTVKAICTGVINLV 62

Db 2 NWATFQOKHIINTPIICNTIMDNNIYIVGGCKRVNTFIISATTVKAICTGVINNV 61

QY 63 TTRFQNLCTCTRTSIPTPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

Db 62 TTRFQNLCTCTRTSIPTPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110

RESULT 7

AAV33321

ID AAY33321 standard; protein; 111 AA.

XX AAY33321;

AC AAY33321;

XX 29-NOV-1999 (first entry)

XX Frog lectin protein fragment.

XX Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;

XX heavy chain; cell surface marker; treatment; tumor; viral infection;

XX parasite infection; immune dysfunctional cell; autoimmune disease;

XX contraceptive; cell separation; transplantation; bone marrow ablation;

XX leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.

XX Rana catesbeiana.

OS US5955073-A.

XX 21-SEP-1999.

XX 09-JUL-1997; 97US-00891848.

XX 20-APR-1990; 90US-00510696.

XX 22-OCT-1991; 91US-00779195.

XX 04-FEB-1993; 93US-00014082.

XX 22-SEP-1993; 93US-00125462.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL, Nicholls PJ, Youle RJ;

XX WPI; 1999-560488/47.

XX Recombinantly fused pancreatic RNase-targeting proteins useful for

XX treating tumors, infections, immune or autoimmune disorders and as a

XX contraceptive.

XX Example 3; Fig 19; 47pp; English.

XX This invention describes a novel nucleic acid construct comprising

XX sequences encoding functional pancreatic RNase and a second protein

XX (preferably the light and heavy chains of an antibody) which binds a

XX specific cell surface marker on a target cell and functions as a

XX cytotoxic agent. The products can be used for selectively killing cells

XX expressing a specific surface marker. They can be used for treating

XX tumors or infected cells (e.g. cells infected by viruses (especially

XX latent or chronic virus infections, such as human immunodeficiency virus

XX (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and

XX II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,

XX cytomegalovirus) and cells infected with parasites (such as the malaria

XX parasite). They can also be used for treating immune dysfunctional cells

XX in immune and autoimmune diseases. Additionally, they may be used as

XX contraceptives. Finally they can also be used for cell separation in

XX vitro by selectively killing unwanted types of cells (e.g. in bone

XX marrow) prior to transplantation into a patient undergoing marrow

XX ablation by radiation or for killing leukemia cells or T-cells that would

XX cause graft-versus-host disease. This sequence represents a bullfrog

XX

CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 99.2%; Score 600; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.5e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOOKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 61
 Db 1 QNWATFOOKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
 QY 62 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 Db 61 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4

AAAY28872
 ID AAY28872 standard; protein; 110 AA.

XX
 AC AAY28872;

XX 25-JAN-2000 (first entry)

XX Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.

XX Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.

XX Rana catesbeiana.
 OS Synthetic.

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08130.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 62; 71pp; English.

XX The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases

XX Sequence 110 AA;

Query Match 98.5%; Score 596; DB 2; Length 110;
 Best Local Similarity 98.2%; Pred. No. 1.8e-59;
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOOKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 61
 Db 1 QNWATFOOKHIIINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60
 QY 62 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 Db 61 STTRFQMLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 5

AAAY28878
 ID AAY28878 standard; protein; 111 AA.

XX
 AC AAY28878;

XX 25-JAN-2000 (first entry)

XX Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.

XX Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW CD22; RNase; autoimmune disease.

XX Rana catesbeiana.
 OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

XX WO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US006641.

XX 27-MAR-1998; 98US-0079751P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Rybak SM, Newton DL;

XX WPI; 1999-610847/52.

XX N-PSDB; AAZ08135.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases.

XX Claim 22; Page 68; 71pp; English.

XX The present sequence is a recombinant Rana catesbeiana ribonuclease
 CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
 CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
 CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
 CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
 CC Recombinant ribonucleases can be expressed in bacteria without an N-
 CC terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and

XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)₆
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 605; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.8e-60;
 Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60
 Db 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60
 QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111
 Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111
 RESULT 2
 AAY28873
 ID AAY28873 standard; protein; 111 AA.
 AC AAY28873;
 XX 25-JAN-2000 (first entry)
 DT Recombinant Met (-1) RaCOR1.
 XX Recombinant Met (-1) RaCOR1.
 KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08131.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 63; 71pp; English.
 XX The present sequence is a recombinant Rana catesbeiana oocyte

CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX SQ Sequence 111 AA;
 Query Match 99.3%; Score 601; DB 2; Length 111;
 Best Local Similarity 98.2%; Pred. No. 5e-60;
 Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60
 Db 1 MQNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 60
 QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111
 Db 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRCP 111
 RESULT 3
 AAY28874
 ID AAY28874 standard; protein; 110 AA.
 AC AAY28874;
 XX 25-JAN-2000 (first entry)
 DT Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
 XX Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
 KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX Rana catesbeiana.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 22 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 57 /note= "Wild type Met replaced with Leu"
 XX WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Rybak SM, Newton DL;
 XX WPI; 1999-610847/52.
 XX N-PSDB; AAZ08132.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 64; 71pp; English.
 XX The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal


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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OX Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE.
RP TISSUE=Milk, and Serum;
RX MEDLINE=97409980; PubMed=9266695;
RA Strydom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RL Eur. J. Biochem. 247:535-544 (1997).
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; P10152; IAGI.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyridoxone carboxylic acid. PYROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
FT SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 123;
Best Local Similarity 29.6%; Pred. No. 1.8e-06;
Matches 32; Conservative 20; Mismatches 43; Indels 13; Gaps 5;

OY 6 FQKHIIPT-----ICNTILDNNIYVGQCKRVNTFISSATTVKAIC---TGVINL 57
DB 8 FLRKHYPSPGTHDDRYCNYTWERR--NMTRPCKDTNTFIHNSDDIRAVCDRNGEPYR 65

OY 58 NVLSTTR--FQNTCTRTSITPR-PCPYSSRTETNYICVKCE--NOY-PVHFA 102
DB 66 NGLRSRSPFQVTTCHRRGSGRPFCRYRFRANRVIVIRCDDGFPPIH 113

RESULT 14
RNBR_GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Giraffa camelopardalis (Giraffe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC Giraffidae; Giraffa.
OX NCBI_TaxID=9894;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species.";
RL J. Mol. Evol. 41:850-858 (1995).

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RN [2]
RN SEQUENCE OF 31-114 FROM N.A.
RX MEDLINE=93367815; PubMed=8360916;
RA Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RL J. Mol. Evol. 37:29-35 (1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC EMBL; S81743; AAB36137.1; -.
CC EMBL; S65126; AAB27931.1; -.
CC HSP; P00656; 2RNS.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC PRODOM; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...). (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT SEQUENCE 141 AA; 15592 MW; 73745E9E9079591F CRC64;

Query Match 20.6%; Score 123.5; DB 1; Length 141;
Best Local Similarity 29.8%; Pred. No. 2.1e-06;
Matches 36; Conservative 18; Mismatches 44; Indels 23; Gaps 7;

OY 4 ATFOQKH-----INTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINL 57
DB 6 AKFRHMDSGSSSSSSNSNVCNMKRR-RWTHRCAPVNTFVHESLADYKAVCS---QK 61

OY 58 NVL-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKCE--NOY-PVHFA 104
DB 62 NIICKNGQPCYQSNSTMTNITDCRETGSSKYPCAYKTSQKYITVACGPNYPVPHFD 121

OY 105 G 105
DB 122 G 122

RESULT 15
RNBR_AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=98278842; PubMed=9611269;
RA Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,

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Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

QY 4 ATFOOKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINL 57
 |:::|
 Db 32 AKFRQHMDSGSSSGNPNYCNQMRR-RMTHGRCKPVNTFVHESLDDVKAACS---QK 87
 |:::|
 QY 58 NVL-----STTRFQMTCTRTSITPRP-CFYSRSTETNYICVKCE-NQY-PVHFA 104
 |:::|
 Db 88 NITCKNGHPNCYQSKSTWSTDCRETGSSKYPNCAYTSOKQYITVACEGNPVPVHFD 147
 |:::|
 QY 105 G 105
 Db 148 G 148

RESULT 11
 RNP_IGUIG
 ID RNP_IGUIG STANDARD; PRT; 119 AA.
 AC PR0287; 1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 OS Iguana iguana (Common iguana).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosaurs; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=8517;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=94139745; PubMed=8307028;
 RA Zhao W., Beintema J.J., Hofsteenge J.;
 RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
 ribonuclease."
 RL Eur. J. Biochem. 219:641-646 (1994).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pancreas.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR; S41111; S41111.
 DR HSSP; P00656; ILSQ.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; RNaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Pyrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 25 80 BY SIMILARITY.
 FT DISULFID 39 91 BY SIMILARITY.
 FT DISULFID 57 106 BY SIMILARITY.
 FT ACT_SITE 10 10 BY SIMILARITY.
 FT ACT_SITE 40 40 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 21.2%; Score 127.5; DB 1; Length 119;
 Best Local Similarity 29.6%; Pred. No. 6.5e-07;
 Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

QY 1 QNATFOOKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAIC-- 51
 |:::|
 Db 1 QDSSSFQKHIDYPTSAASNPAYCDLMMQR-NLNPYCKTRNTFVHASPEIQOVCS 59
 |:::|
 QY 52 --TGVINLVSTTRFQMTCTRTSIT-PRPCYSSRTETNYICVKCENQYVPVHF 103
 |:::|
 Db 60 GGTHTEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTGTGKRIACENQVPVHF 114
 |:::|

RESULT 12

RNBR_CAPCA
 ID RNBR_CAPCA STANDARD; PRT; 151 AA.
 AC P79351;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
 OS Capreolus capreolus (Roe deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Odocoileinae; Capreolus.
 OX NCBI_TaxID=9858;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278842; PubMed=9611269;
 RA Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
 RA Beintema J.J.;
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants."
 RL Gene 212:259-268 (1998).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; Y11673; CAA72371.1; -.
 DR HSSP; P00656; ILSRN.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; RNaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
 FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
 FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
 SQ SEQUENCE 151 AA; 16971 MW; 392D0E6302F006A6 CRC64;

Query Match 20.8%; Score 124.5; DB 1; Length 151;
 Best Local Similarity 28.6%; Pred. No. 1.8e-06;
 Matches 34; Conservative 18; Mismatches 44; Indels 23; Gaps 6;

QY 4 ATFOOKHI-----INTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINL 57
 |:::|
 Db 6 AKFRQHMDSGSSSGNPNYCNQMRR-RMTHGRCKPVNTFVHESLDDVKAACS---QK 61
 |:::|
 QY 58 NVL-----STTRFQMTCTRTSITPRP-CFYSRSTETNYICVKCENQ--YVPHF 103
 |:::|
 Db 62 NITCKNGHPNCYQSKSTWSTDCRETGSSKYPNCAYTSOKQYITVACEGDPVPVHFD 120
 |:::|

RESULT 13
 ANG2_BOVIN
 ID ANG2_BOVIN STANDARD; PRT; 123 AA.
 AC P80929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-2 (EC 3.1.27.-).
 GN ANG2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gastra W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The
RT disulfide bonds.";
RL J. Biol. Chem. 245:654-661 (1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphogluconolactides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR: A92071; NRRG.
DR HSP; P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF000074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT SIGNAL 26
FT DISULFID 84
FT FT 26
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT CARBOHYD 76 76
FT SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;
KW Query Match 21.6%; Score 129.5; DB 1; Length 124;
Best Local Similarity 30.7%; Pred. No. 4.1e-07;
Matches 35; Conservative 20; Mismatches 42; Indels 17; Gaps 6;
QY 6 FQOKHI-----INTPIICNTILDNNIYVGQCKRVNTFIISATTVAICTGV-INLN 58
DB 8 FORQHMDFDSSSSNSNVCNLMMSRR-NMTQGRCKPVTNFHESLADYQAVCSQINVCK 66
QY 59 VLSTTRFQNLN-----CTRTSITPRP-CPXSSRTETNYICVKBNQ--YPVHF 103
DB 67 NGQTCNYQSNSTMTHTDCRQTGSSKVPNCAYKASQEQKHIIIVACRGNPPVPVHF 120
RESULT 10
RNRB BOVIN
ID RNRB BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
GN BRN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92093604; PubMed=1754384;
RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
RA Viola M., Palmieri M., Russo E., Furia A.;
RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
RT and its expression in different regions of the brain.";
RL Nucleic Acids Res. 19:6469-6474 (1991).
RN [2]
RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
RX TISSUE=Brain;
RX MEDLINE=89214015; PubMed=3243767;
RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
RA Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bovine brain.";
RL J. Biochem. 104:939-945 (1988).
RN [3]
RP SEQUENCE OF 27-167 FROM N.A.
RX MEDLINE=96139017; PubMed=8587129;
RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RT "Molecular evolution of genes encoding ribonucleases in ruminant
RT species";
RL J. Mol. Evol. 41:850-858 (1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
EMBL; X59767; CAA42439.1; -.
EMBL; S81744; AAB36138.1; -.
PIR; S20066; S20066.
HSP; P00656; 2RNS.
GlycoSuiteDB; P39873; -.
InterPro: IPR001427; RNaseA.
Pfam; PF000074; RNaseA; 1.
PRINTS; PR00794; RIBONUCLEASE.
ProDom; PD000535; RNaseA; 1.
SMART; SM00092; RNase_Pc; 1.
PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .).
FT FTID=CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;
Query Match 21.6%; Score 129.5; DB 1; Length 167;
Best Local Similarity 30.6%; Pred. No. 5.7e-07;

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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S., Krzyzinski M.I., Skalska U., Smalus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP PARTIAL SEQUENCE.
 RC TISSUE=Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RA "Characterization and sequencing of rabbit, pig and mouse
 RT angiotensins: discernment of functionally important residues and
 RT regions.";
 RL Biochim. Biophys. Acta 1162:177-186 (1993).
 CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
 CC to actin on the surface of endothelial cells; once bound,
 CC angiotensin is endocytosed and translocated to the nucleus, thereby
 CC promoting the endothelial invasiveness necessary for blood vessel
 CC formation. Angiotensin induces vascularization of normal and
 CC malignant tissues. Abolishes protein synthesis by specifically
 CC hydrolyzing cellular tRNAs.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
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 CC
 CC EMBL; U22516; AAA91366.1; -;
 CC EMBL; BC055355; AAH5355.1; -;
 CC PIR; A35932; A35932.
 CC HSP; P03950; 1A4Y.
 CC MGD; MG1:88022; Ang.
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNase_Pc; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 145 ANGIOENIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT ACT_SITE 37 37 BY SIMILARITY.
 FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
 Query Match 22.8%; Score 136.5; DB 1; Length 145;
 Best Local Similarity 40.3%; Pred. No. 8.6e-08;
 Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;
 QY 33 CKRVNFTFISSATTVKAICTG-----VINLVNLTSTRFQNTCTRTSITPR-PCPYSSRT 86

Db 63 CKDVNTFHGKSNKAIKANGSPYRENLR-MSKSPFQVTTCKHTGGSPRPCCQVRSA 121
 QY 87 ETNYICVKCENQYVHF 103
 Db 122 GFRHVVIACENGLPVHF 138
 RESULT 8
 RNP_BALAC
 ID_RNP_BALAC STANDARD; PRT; 124 AA.
 AC PC0673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 GN RNASE1 OR RNS1.
 OS Balaenoptera acutorostrata (Minke whale) (lesser rorqual).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 CC Balaenopteridae; Balaenoptera.
 CC NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277855; PubMed=9628770;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RT ribonuclease.";
 RL Biochem. J. 157:317-323 (1976).
 CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Pancreas.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC PIR; A00818; NRWHK.
 DR HSP; P00656; 1SRN.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; RNaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 DR Hydrolase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT ACT_SITE 119 119 BY SIMILARITY.
 FT CARBOHYD 76 76 N-LINKED (GLCNAC...) (30%).
 SQ SEQUENCE 124 AA; 14125 MW; F57475459P697E20 CRC64;
 Query Match 21.9%; Score 131.5; DB 1; Length 124;
 Best Local Similarity 32.5%; Pred. No. 2.5e-07;
 Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;
 QY 6 FQQRHII-----NTPIICNTILDNNIYIVGGCKRVNTFISSATTVKAICTGVINLV 59
 Db 8 FQRQHMDSGNSPCNNPNYCNQMMRR-KMTQGRCKPVNTFVHESLEDVKVCS---QKNV 63
 QY 60 L-----SITRFQNTCTRTSITPR-PCPYSSRTETNYICVKE-NQY-PVHF 103
 Db 64 LCKNGRTNCTYESNSTMHTDCRQTGSSKYPNCAYKTSQEKHIIIVACEGPNYPVHF 120
 RESULT 9
 RNP_PIG
 ID_RNP_PIG STANDARD; PRT; 124 AA.
 AC P00671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)


```

CC residues with a 3'-flanking guanine. Hydrolyzes poly(U) and poly(C)
CC as substrates, and prefers the former. The S-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin. It is cytotoxic against several tumor cells.
CC
CC SUBUNIT: Monomer.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
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CC
CC -----
CC EMBL; AF039104; AAD10702.1; -.
CC
CC PIR; A27121; A27121.
CC
CC PDB; 1BC4; 28-OCT-98.
CC
CC PDB; 1M07; 21-JAN-03.
CC
CC InterPro; IPR001427; RNaseA.
CC
CC Pfam; PF00074; rnaseA; 1.
CC
CC ProDom; PD000535; RNaseA; 1.
CC
CC SMART; SM00092; RNase_Pc; 1.
CC
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC
CC Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
CC KW Signal; Pyrrolidone carboxylic acid.
CC
CC FT CHAIN 1 22 RIBONUCLEASE, OOCVTES.
CC FT MOD_RES 23 133 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 23 23
CC FT ACT_SITE 32 32
CC FT ACT_SITE 57 57
CC FT ACT_SITE 125 125
CC FT ACT_SITE 125 125
CC FT DISULFID 41 93
CC FT DISULFID 56 103
CC FT DISULFID 74 118
CC FT DISULFID 115 132
CC FT DISULFID 125 32
CC FT HELIX 25 32
CC FT HELIX 41 45
CC FT TURN 48 49
CC FT STRAND 59 63
CC FT STRAND 63 73
CC FT HELIX 74 74
CC FT TURN 77 74
CC FT STRAND 79 84
CC FT STRAND 90 95
CC FT STRAND 105 110
CC FT STRAND 114 119
CC FT TURN 120 121
CC FT STRAND 122 129
CC FT STRAND 133 133
CC FT SEQUENCE 133 AA; A7D62594F7D16F0C CRC64;
CC
CC Query Match 97.6%; Score 585.5; DB 1; Length 133;
CC Best Local Similarity 97.3%; Pred. No. 3.6e-56;
CC Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
CC
CC QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 59
CC |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||:
CC DB 23 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNV 82
CC
CC QY 60 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
CC |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 83 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 133
CC
CC RESULT 2
CC LECs_RANJA STANDARD; PRT; 111 AA.
CC AC P18839;
CC DT 01-NOV-1990 (Rel. 16, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 10-OCT-2003 (Rel. 42, Last annotation update)

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DE Sialic acid-binding lectin (EC 3.1.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RN SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RC MEDLINE=91035319; PubMed=22290005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,
RA Takayanagi Y., Tani K.,
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: The S-lectins in frog eggs may be involved in the
CC fertilization and development of the frog embryo. This lectin
CC preferentially agglutinate a large variety of tumor cells, but it
CC does not agglutinate non-transformed cells and erythrocytes.
CC
CC -1- SUBUNIT: Monomer.
CC
CC -1- SUBCELLULAR LOCATION: Secreted.
CC
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC
CC PIR; JX0120; JX0120.
CC
CC HSP; P11916; IBC4.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaseA; 1.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNase_Pc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;
CC KW Pyrrolidone carboxylic acid.
CC FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
CC FT ACT_SITE 10 10 BY SIMILARITY.
CC FT ACT_SITE 35 35 BY SIMILARITY.
CC FT ACT_SITE 104 104 BY SIMILARITY.
CC FT DISULFID 19 72
CC FT DISULFID 34 82
CC FT DISULFID 52 97
CC FT DISULFID 94 111
CC FT SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;
CC
CC Query Match 75.2%; Score 451; DB 1; Length 111;
CC Best Local Similarity 77.5%; Pred. No. 9e-42;
CC Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;
CC
CC QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
CC |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 1 QNWAKFOEKHPTNSINCNITMDKSIYVGGQCKERTFISSATTVKAICSGASTNRN 60
CC
CC QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRGC 109
CC |||||||||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||
CC DB 61 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENRUPVHFAGIGRGC 111
CC
CC RESULT 3
CC RNPL_RANJA STANDARD; PRT; 111 AA.
CC ID RNPL_RANJA STANDARD; PRT; 111 AA.
CC AC P14626;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Ribonuclease, liver (EC 3.1.1.27.5).
CC OS Rana catesbeiana (Bull frog).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
CC OX NCBI_TaxID=8400;
CC RN [1]
CC RN SEQUENCE.
CC RP TISSUE=Liver;
CC RX MEDLINE=90130374; PubMed=2613682;
CC RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
CC RA Okazaki T., Ohgaki K., Irie M.;
CC RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
CC liver."

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.55659 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-19

Perfect score: 600

Sequence: 1 QNWFQKHIIINTPIICNT.....ICVKENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	585.5	97.6	133	1	RNPO_RANCA
2	451	75.2	111	1	LECS_RANJA
3	370	61.7	111	1	RNPL_RANCA
4	273.5	45.6	104	1	RN30_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	131.5	21.9	124	1	RNP_BALAC
9	129.5	21.6	124	1	RNP_PIG
10	129.5	21.6	167	1	RNBR_BOVIN
11	127.5	21.2	119	1	RNP_IGUIG
12	124.5	20.8	151	1	RNBR_CAPCA
13	123.5	20.6	123	1	ANG2_BOVIN
14	123.5	20.6	141	1	RNBR_GIRCA
15	123.5	20.6	141	1	RNBR_AXIPR
16	123	20.5	146	1	ANGI_MIOTA
17	123	20.5	146	1	ANGI_SAISC
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	119.5	19.9	143	1	RNBR_SHEEP
21	119	19.8	122	1	RNP_MACRU
22	118.5	19.8	123	1	ANGI_PIG
23	118.5	19.8	124	1	RNP_ANTAM
24	118	19.7	146	1	ANGI_AOTTR
25	117	19.5	146	1	ANGI_SAGOE
26	116.5	19.4	128	1	RNP_MYOCO
27	116.5	19.4	149	1	RNP_MOUSE
28	115	19.2	146	1	ANGI_MACMU
29	114.5	19.1	128	1	RNBR_CAVPO
30	114	19.0	148	1	ANGI_BOVIN
31	113.5	18.9	124	1	RNP_CANDR
32	113.5	18.9	128	1	RNP_HORSE
33	113	18.8	147	1	ANGI_HUMAN

34	113	18.8	147	1	ANGI_PANTR
35	112.5	18.8	119	1	RNS4_BOVIN
36	112.5	18.8	128	1	RNP_PROGU
37	109.5	18.2	124	1	RNP_RANTA
38	109.5	18.2	146	1	ANGI_PAPHA
39	109.5	18.2	148	1	RNS4_MOUSE
40	109	18.2	125	1	ANGI_RABIT
41	108.5	18.1	124	1	RNP_CAPCA
42	108.5	18.1	124	1	RNP_GIRCA
43	108.5	18.1	130	1	RNP_CRILLO
44	107.5	17.9	124	1	RNP_BUBBU
45	107.5	17.9	148	1	RNP_PERLE

ALIGNMENTS

RESULT 1
RNPO_RANCA STANDARD; PRT; 133 AA.
AC PII916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
[1]
SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease. Tissue distribution, cloning, purification, cytotoxicity, and active residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
[2]
SEQUENCE OF 23-133.
RP TISSUE=Egg;
RC MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H., Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
[3]
CHARACTERIZATION, AND SEQUENCE OF 81-101.
RC MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
[4]
CHARACTERIZATION.
RC TISSUE=Egg;
RC MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H., Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
[5]
STRUCTURE BY NMR OF 23-133.
RC MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
J. Mol. Biol. 283:231-244(1998).
CC -!- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

Search completed: May 7, 2004, 21:54:56
Job time : 10.9813 secs

Db 7 FQHQHMDTEHSTASSNYCNLMKAR-DMTSGRCKPLNTFIHPEKSVVDVACHOENVTK 65

QY 52 TGVINLVSTTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKENQY-PVHF 103

Db 66 NGRNTNC-YKSNRLSITNCRTQASKYPNCQYETSNLNKQIIVACEGQVYPVHF 118

RESULT 11

A43825

angiogenin - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S29834; A43825

R:Bond, M.D.; Strydom, D.J.; Vallée, B.L.

R:Biochim. Biophys. Acta 1162, 177-186, 1993

A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: disclermined

A:Reference number: S29833; MUID:93192291; PMID:8448162

A:Accession: S29834

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-123 <SON>

A:Note: this sequence was submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

Query Match 19.8%; Score 118.5; DB 1; Length 123;

Best Local Similarity 39.5%; Pred. No. 9.3e-05;

Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

QY 33 CKRVNTFIISATTVKAICTG-----VINLVSTTRFQNLCTRTSTITPR-PCPYSSRTE 87

Db 39 CKEVNTFHGRNDIKAIKNDKNGEPYNNFRSKSPFOITCKHKGSGNRPFCGYRATAG 98

QY 88 TNYICVKENQYYPVHF 103

Db 99 PRTIACVACENGLPVHF 114

RESULT 12

NRPH

pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Antilocapra americana (pronghorn)

C>Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000

C:Accession: A00813

R:Beintema, J.J.; Gastra, W.; Munniksma, J.

J. Mol. Evol. 13, 305-316, 1979

A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship between

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BE>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 19.8%; Score 118.5; DB 1; Length 124;

Best Local Similarity 29.9%; Pred. No. 9.3e-05;

Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;

QY 4 ATPQKHITPI-----ICNTILDNNIYVGGQCKRVNTFIISATTVKAICT----- 52

Db 6 AKFEROHIDNSVSSVSSNYCNQMKSR-NLTGGRCKPNTFVHESLADVQAVCSQKVA 64

QY 53 ---GVINLVSTTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103

Db 65 CKNGQINC-YQSYSTYSITDCRTGSSKYPNCAYKTQAKKHIIVACEGPNYPVPHY 120

RESULT 13

NRPU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Myocastor coypus (nutria, coypu)

C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000

C:Accession: A00822

R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.

R:Biochim. Biophys. Acta 453, 400-409, 1976

A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic

A:Reference number: A90612; MUID:77065676; PMID:999896

A:Accession: A00822

A:Molecule type: protein

A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 116.5; DB 1; Length 128;

Best Local Similarity 30.8%; Pred. No. 0.00015;

Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 6 FQOKHI-----INTPLICTNLDNNIYVGGQCKRVNTFIISATTVKAICTGVINLV 59

Db 8 FERQHMDSRGSPSTPNYCNEMKSR-NMTQGRCKPNTFVHEPLADVQAVC---FQKNV 63

QY 60 L-----STTRFQNLCTRTSTITPRP-CPYSSRTETNYICVKE-NQY-PVHF 103

Db 64 LCKNGQINCYSNSNMHITDCRVTSNSDYPCNSYRTSQEEKSIIVACEGPNYPVPHF 120

RESULT 14

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse

N:Alternate names: RNase 1; RNase A

C:Species: Mus musculus (house mouse)

C>Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: A34090; S22598; A00830

R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.

Mol. Biol. Evol. 7, 29-44, 1990

A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse

A:Reference number: A34090; MUID:90136034; PMID:2299980

A:Accession: A34090

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <SCH>

A:Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763

R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.

Nucleic Acids Res. 19, 6935-6941, 1991

A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific

A:Reference number: S22598; MUID:92107684; PMID:1840677

A:Accession: S22598

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-149 <SAM>

A:Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982

R:Lenstra, J.A.; Beintema, J.J.

Eur. J. Biochem. 98, 399-408, 1979

A:Title: The amino acid sequence of mouse pancreatic ribonuclease.

A:Reference number: A00830; MUID:80024269; PMID:556267

A:Accession: A00830

A:Molecule type: protein

A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>

F:37,66,144/Active site: His, Lys, His #status predicted

F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted

F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 116.5; DB 1; Length 149;

Best Local Similarity 29.9%; Pred. No. 0.00018;

Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;

```

; ;Molecule type: protein
; ;Residues: 27-154,'S',156-166 <WAT>
; ;Experimental source: brain
; ;Superfamily: pancreatic ribonuclease
; ;Keywords: glycoprotein; hydrolase
; ;52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted
; ;38,67,145/Active site: His, Lys His
; ;88/Binding site: carbohydrate (Asn)
; ;155/Binding site: carbohydrate (Thr)
; ;159/Binding site: carbohydrate (Ser)

```

[illegible]

QY 1 QNWATFOQKHINTP-IIQNTILDNNIYVGGCKRVNTFISSATTVKAICTGV-INLN 58
 DB 1 QNWAKFQKHINTPNTSINCNTIMDKSIYVGGCKERNFTFISSATTVKAICSGASTNRN 60
 QY 59 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHFAGIGRC 109
 DB 61 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHFAGIGRC 111
 RESULT 3
 JX0085
 pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
 C:Species: Rana catesbeiana (bullfrog)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
 C:Accession: JX0085
 R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
 J. Biochem. 106, 729-735, 1989
 A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
 A:Reference number: JX0085; MUID:90130374; PMID:2613682
 A:Accession: JX0085
 A:Molecule type: protein
 A:Residues: 1-111 <MIT>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: hydrolase; nucleic acid degradation; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:10,35,104/Active site: His, Lys, His #status predicted
 F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted
 Query Match 61.7%; Score 370; DB 2; Length 111;
 Best Local Similarity 64.9%; Pred. No. 1.1e-29;
 Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;
 QY 1 QNWATFOQKHINTP-IIQNTILDNNIYVGGCKRVNTFISSATTVKAICTGV-INLN 58
 DB 1 QNWAKFQKHINTPNTSINCNTIMDKSIYVGGCKERNFTFISSATTVKAICSGASTNRN 60
 QY 59 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHFAGIGRC 109
 DB 61 ELSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHFAGIGRC 111

RESULT 4
 A39035
 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
 C:Species: Rana pipiens (northern leopard frog)
 C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
 C:Accession: A39035
 R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
 J. Biol. Chem. 266, 245-251, 1991
 A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
 A:Reference number: A39035; MUID:91093131; PMID:1985896
 A:Accession: A39035
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-104 <ARD>
 C:Superfamily: pancreatic ribonuclease
 Query Match 45.1%; Score 270.5; DB 2; Length 104;
 Best Local Similarity 47.7%; Pred. No. 7.1e-20;
 Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;
 QY 1 QNWATFOQKHINTP-IIQNTILDNNIYVGGCKRVNTFISSATTVKAICTGV-INLN 58
 DB 1 EDWLTFOQKHINTPNTSINCNTIMDKSIYVGGCKERNFTFISSATTVKAICSGASTNRN 56
 QY 59 VLSTTRFQNTCTRTSITPRPCPSYSSRTETNYICVKCENQYVHFAGIGRC 109
 DB 57 VLTTSFYLSDC---NVTSPCKYKLKSKNFKVCVENCQAPVHFVGVGSC 104

RESULT 5
 A35932
 angiogenin precursor - mouse

N:Alternate names: angiogenesis factor
 N:Contains: ribonuclease (EC 3.1.27.-)
 C:Species: Mus musculus (house mouse)
 C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
 C:Accession: A35932
 R:Bond, M.D.; Vallee, B.L.
 Biochem. Biophys. Res. Commun. 171, 988-995, 1990
 A:Title: Isolation and sequencing of mouse angiogenin DNA.
 A:Reference number: A35932; MUID:91025023; PMID:222458
 A:Accession: A35932
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-145 <BON>
 A:Cross-references: GB:U22516; NID:G726325; PIDN:AAA91366.1; PID:G726326
 C:Genetics:
 A:Introns: #status absent
 C:Function:
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
 F:1-24/Domain: signal sequence #status predicted <SIG>
 F:25-145/Product: angiogenin #status predicted <MAT>
 F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F:37,64,137/Active site: His, Lys, His #status predicted
 F:50-104,63-115,81-130/Disulfide bonds: #status predicted
 Query Match 22.8%; Score 136.5; DB 1; Length 145;
 Best Local Similarity 40.3%; Pred. No. 1.8e-06;
 Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;
 QY 33 CKRVNTPFISSATTVKAICTG-----VINLVLTSTFQNTCTRTSITPR-PCPYSSRT 86
 DB 63 CKDVTTFHGNKSNKAIKANGSPYRENL-RMSKSPFQVTKHTGGSPRPPCQYRASA 121
 QY 87 ETNYICVKCENQYVHF 103
 DB 122 GFRHVITACENGLPVHF 138
 RESULT 6
 NRWHK
 pancreatic ribonuclease (EC 3.1.27.5) - minke whale
 N:Alternate names: RNase A
 C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
 C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
 C:Accession: A00818
 R:Emmens, M.; Welling, G.W.; Beintema, J.J.
 Biochem. J. 157, 317-323, 1976
 A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
 A:Reference number: A00818; MUID:76277855; PMID:962870
 A:Accession: A00818
 A:Molecule type: protein
 A:Residues: 1-124 <EMM>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
 F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 Query Match 21.9%; Score 131.5; DB 1; Length 124;
 Best Local Similarity 32.5%; Pred. No. 4.8e-06;
 Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;
 QY 6 FQKHII-----NTPFIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLVN 59
 DB 8 FQKHII-----NTPFIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLVN 59
 QY 60 L-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKE-NQY-PVHF 103
 DB 64 LCKNGRTNCSNENSTMTHTDCRQTGSSKYPNCAKTSQKEKHIIIVACENGVFVPHF 120
 RESULT 7

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

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Run on: May 7, 2004, 21:38:36 ; Search time 9.98129 Seconds
        (without alignments)
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Title: US-09-961-400-19
 Perfect score: 600
 Sequence: 1 QNWATFQKHINTPIICNT.....ICVKCNQYVHPFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2833366

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	582.5	97.1	111	2	A27121	ribonuclease-relat
2	451	75.2	111	1	JX0120	ribonuclease-relat
3	370	61.7	111	1	JO0085	pancreatic ribonuc
4	270.5	45.1	104	2	A39035	ribonuclease-relat
5	136.5	22.8	145	1	A35932	ribonuclease-relat
6	131.5	21.9	124	1	NRWHK	angiogenin precurs
7	129.5	21.6	124	1	NRPG	pancreatic ribonuc
8	129.5	21.6	167	2	S20066	pancreatic ribonuc
9	127.5	21.2	119	2	S41111	pancreatic-type ri
10	119	19.8	122	1	NRKGR	pancreatic ribonuc
11	118.5	19.8	123	1	A43825	pancreatic ribonuc
12	118.5	19.8	124	1	NRPRH	angiogenin - pig
13	116.5	19.4	128	1	NRPU	pancreatic ribonuc
14	116.5	19.4	149	1	NPMS	pancreatic ribonuc
15	114.5	19.1	128	1	NRGPB	pancreatic ribonuc
16	114	19.0	125	1	A32474	pancreatic ribonuc
17	113.5	18.9	124	1	NRCM	angiogenin lvalida
18	113.5	18.9	124	1	NRCVM	pancreatic ribonuc
19	113.5	18.9	124	1	NRCMB	pancreatic ribonuc
20	113.5	18.9	128	1	NPHO	pancreatic ribonuc
21	113	18.8	147	1	NRHUAG	pancreatic ribonuc
22	112.5	18.8	128	1	NRKS	pancreatic ribonuc
23	110.5	18.4	124	2	S08549	angiogenin precurs
24	109.5	18.2	124	1	NFDEN	pancreatic ribonuc
25	109	18.2	125	1	B43825	ribonuclease - dom
26	108.5	18.1	124	1	NRGF	pancreatic ribonuc
27	108.5	18.1	124	1	NRDEO	angiogenin - rabbi
28	108.5	18.1	130	2	S22808	pancreatic ribonuc
29	107.5	17.9	124	1	NRWB	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
 ribonuclease-related sialic acid-binding lectin - bullfrog
 C:Species: *Rana catesbeiana* (bullfrog)
 C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_of_revision 1
 C:Accession: A27121
 R:Titani, K.; Takito, K.; Kuwada, M.; Nitta, K.; Sakakibara, Y.
 Biochemistry 26, 2189-2194, 1987
 A:Title: Amino acid sequence of sialic acid-binding lectin from *Rana catesbeiana*
 A:Reference number: A27121; MUID:87299649; PMID:3304421
 A:Accession: A27121
 A:Molecule type: protein
 A:Residues: 1-111 <TR>
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: lectin

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 1e-50;
Matches 107; Conservative 3; Mismatches 0; Indels 1

Qy	1	QNWATFOQKHINTPII-NTILDNNIYVIGQCKRVNTFIISATTVKAICTGVINLV	59
Db	1	ENWATFOQKHINTPII-NCNTIMDNNIYVIGQCKRVNTFIISATTVKAICTGVINLV	60
Qy	60	LSLTFPQNTCRTSITPRCPYSSKRTETNYICVKCENQYPVHFAGICRCP	110
Db	61	LSLTFPQNTCRTSITPRCPYSSKRTETNYICVKCENQYPVHFAGICRCP	111

RESULT 2

ribonuclease-related stialic acid-binding lectin - Japanese frog
C:Species: *Rana japonica* (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takaya, K.
A:Title: Amino acid sequence of a lectin from Japanese frog (*Rana japonica*) eggs.
A:Reference number: JX0120; PMID:91035319; PMID:2229005
A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:19-72,94-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.2%; Score 451; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 1e-37;
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

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;
;  OTHER INFORMATION: /label= Onc
;  OTHER INFORMATION: /note= "Onconase from Rana pipiens"
US-08-891-848-13

Query Match      45.1%; Score 270.5; DB 2; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

QY  1 QNWATFOQKHINT-PIICNTILDNNIYIVGGCKRWNTFIISATTVKAITGVINLN 58
      :: ||| ||| ||| ||| ||| :: ||| ||| ||| ||| ||| :: ||| |||
DB  1 EDWLTFOQKHINTRDVDCDINMTNLF---HCKKNVFIYRPERPVKAIKGIATSKN 56
      :: ||| ||| ||| ||| ||| :: ||| ||| ||| ||| ||| :: ||| |||

QY  59 VLSTTRFQLNTCTRITSPPCPYSRSETNYTCVKENCQYPVHFAIGRC 109
      ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||
DB  57 VLTTSFYLSDC---NVTSRPCKYKLSKSTNKFVCVCENQAPVHFVGVCSC 104
      ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: ||| :: |||

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Job time : 13.7596 secs

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Search completed: May 7, 2004, 21:40:46
Job time : 13.7596 secs

RESULT 15
 US-08-891-848-13
 ; Sequence 13, Application US/08891848
 ; Patent No. 5955073
 ; GENERAL INFORMATION:
 ; APPLICANT: Rybak, Susanna M.
 ; APPLICANT: Youle, Richard J.
 ; APPLICANT: Newton, Dianne L.
 ; APPLICANT: Nicholls, Peter J.
 ; TITLE OF INVENTION: Selective Rhase Cytotoxic Reagents
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/891.848
 ; FILING DATE: No. 5955073 yet assigned
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/125,462
 ; FILING DATE: 22-SEP-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/014,082
 ; FILING DATE: 04-FEB-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/779,195
 ; FILING DATE: 22-OCT-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/510,696
 ; FILING DATE: 20-APR-1990
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Ellen Lauver
 ; REGISTRATION NUMBER: 32,762
 ; REFERENCE/DOCKET NUMBER: 015280-110310US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 104 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..104

Sat May 8 17:57:17 2004

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; DEVELOPMENTAL STAGE: Embryo
;
US-08-283-971-1
Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAITGVINLN 58
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 1 EDWLTFQKHINTRDVDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSTTRPQNTCTRTSITPRPCPSYRSRTETNYICVKCENQYVHFAGIGRC 109
   |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 57 VLATSEFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFGVGVGSC 104

RESULT 13
US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/921,619
; FILING DATE: 19920728
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5005 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5595734 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
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; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
;
US-07-921-619-1
Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 6.5e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAITGVINLN 58
   :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 1 EDWLTFQKHINTRDVDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56

QY 59 VLSTTRPQNTCTRTSITPRPCPSYRSRTETNYICVKCENQYVHFAGIGRC 109
   |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
Db 57 VLATSEFYLSDC---NVTSPCKYKUKKSTNKFVCVCENQAPVHFGVGVGSC 104

RESULT 14
US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-63

Query Match 45.6%; Score 273.5; DB 3; Length 129;
Best Local Similarity 48.6%; Pred. No. 3.8e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 26 QDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIATSKN 81
QY 59 VLSTTRFQMLNCTRTSTITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 82 VLTTSFYLSDC---NVTSPCKYKUKSTNKFVCVCENQAPVHFVGVGSC 129

RESULT 11
US-08-875-811-43
; Sequence 43, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
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; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 379 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-43

Query Match 45.6%; Score 273.5; DB 3; Length 379;
Best Local Similarity 48.6%; Pred. No. 1.4e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOOKHIINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
Db 26 QDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIATSKN 81
QY 59 VLSTTRFQMLNCTRTSTITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 82 VLTTSFYLSDC---NVTSPCKYKUKSTNKFVCVCENQAPVHFVGVGSC 129

RESULT 12
US-08-283-971-1
; Sequence 1, Application US/08283971
; Patent No. 5529775
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; APPLICANT: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,971
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,180
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5006 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5529775 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
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us-09-961-400-19.ral

Sat May 8 17:57:17 2004

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;
; APPLICANT: Ardelt, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,429
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/626,288
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-095-429-1

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKATCTGVI-NLN 58
Db 1 QDWLTFOQKHITNTRDVDCDNIINSTLNF----HCKDKNTFIYSRPEPVKAIKGLIASKN 56

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLKSTNKFVCVTCENQAPVHFVGVGSC 104

RESULT 10
US-08-875-811-63
; Sequence 63, Application US/08875811
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;
; APPLICANT: Ardelt, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,288
; FILING DATE: No. 6649392 yet assigned
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-626-288-1

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKATCTGVI-NLN 58
Db 1 QDWLTFOQKHITNTRDVDCDNIINSTLNF----HCKDKNTFIYSRPEPVKAIKGLIASKN 56

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLKSTNKFVCVTCENQAPVHFVGVGSC 104

RESULT 9
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649392
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Boix, Ester
; APPLICANT: Ardelt, Wojciech
; TITLE OF INVENTION: A Mutant Form of Cytotoxic Protein Which
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,288
; FILING DATE: No. 6649392 yet assigned
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Ran, David B.
; REGISTRATION NUMBER: 38,589
; REFERENCE/DOCKET NUMBER: 15280-267
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-626-288-1

Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.9e-24;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKATCTGVI-NLN 58
Db 1 QDWLTFOQKHITNTRDVDCDNIINSTLNF----HCKDKNTFIYSRPEPVKAIKGLIASKN 56

QY 59 VLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTFSEFYLSDC---NVTSPCKYKLKSTNKFVCVTCENQAPVHFVGVGSC 104

RESULT 9
US-09-095-429-1
; Sequence 1, Application US/09095429
; Patent No. 6649392
; GENERAL INFORMATION:
; APPLICANT: Youle, Richard
; APPLICANT: Vasandani, Veena
; APPLICANT: Boix, Ester

```

; DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match	46.8%;	Score 280.5;	DB 1;	Length 104;
Best Local Similarity	48.6%;	Pred. NO. 4.5e-25;		
Matches	54; Conservative	17; Mismatches	31.	Indels

QY	1	ONWATFOOKHINT-PIONTILDNNIYIVGGQCKRVNTLISSATVKAICTGVI-NLN	58
Db	1	EDMLTFOKKVNTFRDVCNNIMSTNLF-----HCKDKNTIYSPPEPVKAICKGIILASKN	56
QY	59	VLSTTRPOLNCTRTSTTPPCPYSSRTNYICVKCENQYPVHFAGIGRC	109
Db	57	VLITSEFYLSDC---NVTSPCKYKLKSTNKFCTVCENQAPVHFVGVRGC	104

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RESULT 4
US-09-394-268-1
; Sequence 1, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; TITLE OF INVENTION: MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1

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Query Match	45.6%	Score 273.5;	DB 3;	Length 104;
Best Local Similarity	48.6%;	Pred. No. 2.9e-24;		
Matches	54; Conservative	16; Mismatches	32; Indels	9

1	ONWATQOQHINT-PIICNTILDNNIYIVGGQCKRVNTEIISATPVKAICTGVI-NLN	58
Qy		
Db		
1	QOWLTQKHHINTROVDCDNIINSTLNF-----HCKKNTIYRPEPVKAIKCGIIASKN	56
Qy		
Db		
59	VLSTRFQINTCWTSITPRPCFYSSRTETNYICVKCENQYPVHFAGICRC	109
Qy		
Db		
57	VLITSEFYIUSDG---NVTSRCPKYKLLKSTNKFVTCENQAPVHFVGVGSC	104
Qy		
Db		

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RESULT 5
US-09-394-268-2
; Sequence 2, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; TITLE OF INVENTION: MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-394-268-2

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Query Match 45.6%; Score 273.5; DB 3; Length 104;
Best Local Similarity 49.5%; Pred. No. 2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy	1	ONWATQOQHIIINT-PIICNTILDNNIYIVGGCKRVNTFISSATTVKAICTGVI-NLN	58
Db	1	QDLWTQKHHIINTRDVDCDNLSTNLF-----HCKDKNTFYRPEPEVKAICKGIIASKN	56
Qy	59	VLSFTTFQIINTCTWISITPRPCYSSRTETNYICVKCNQYVPHFAGIGRC	109
Db	57	VLTTSFYLSDC-----NVTCRCKYLLKSKTNKFCVTENQAPVHFVGVGSC	104

RESULT 6

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US-09-687-748-1
; Sequence 1, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1

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Query Match	45.6%;	Score 273.5;	DB 4;	Length 104;
Best Local Similarity	48.6%;	Pred. No. 2.9e-24;		
Matches 54; Conservative	16;	Mismatches 32.	Indels 0.	Cons 0.

QY	1	QWATFOQKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICGTI-NLN	58
Db	1	QWLFPOKHHIINTRDVDCDNTSMNLF-----HCKDKNTIYRSPREPVKAIKGIISKN	56
QY	59	VLSTRFQIINTCTRTSIPTRPCYSSRTETNYICVKENQYVPHVPGI.GRC	109
Db	57	VLTTFSEFYLSDC--NVTSRPCKYKLLKSTNKFCTVCENQAPVHFVGVGSC	104

RESULT 7

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US-09-687-748-2
; Sequence 2, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
; OTHER INFORMATION: position 72
US-09-687-748-2

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Query Match      45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred.No.2.9e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATGQKHIIINT-PIICNTILNNIIVGGQCKRVNTPFIISATVKAICTGVI-NLN 58
   :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
db 1 QDWTEFKHITIRDVDCDKNITLSTLF-----HCKDKNTFIYRPFEPVKAKIGIISKNI 56
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us-09-961-400-19.ra1

Sat May 8 17:57:17 2004

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;
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-891-848-12

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.4e-60;
Matches 107; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-NTILDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 60

QY 60 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
;

;
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-875-811-8

Query Match 97.1%; Score 582.5; DB 3; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.4e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-NTILDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 59
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVNLNV 60

QY 60 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LSTTRFQNLCTCTSTTPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelit Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 5728805 Applicable
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run On: May 7, 2004, 21:28:45 ; Search time 12.7596 Seconds
(without alignments)
445.066 Million cell updates/sec

Title: US-09-961-400-19
Perfect score: 600
Sequence: 1 QNATFQKHIIPTICNT.....ICVKCENQPVHFAGIGRCP 110

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Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCOTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	97.1	111	2	US-08-891-848-12
2	582.5	97.1	111	3	US-08-875-811-8
3	280.5	46.8	104	1	US-08-467-955-2
4	273.5	45.6	104	3	US-09-394-268-1
5	273.5	45.6	104	3	US-09-394-268-1
6	273.5	45.6	104	4	US-09-687-748-1
7	273.5	45.6	104	4	US-09-687-748-2
8	273.5	45.6	104	4	US-08-626-288-1
9	273.5	45.6	104	4	US-09-095-429-1
10	273.5	45.6	104	4	US-08-875-811-63
11	273.5	45.6	129	3	US-08-875-811-43
12	270.5	45.1	104	1	US-08-283-971-1
13	270.5	45.1	104	1	US-07-921-619-1
14	270.5	45.1	104	1	US-08-467-955-1
15	270.5	45.1	104	2	US-08-891-848-13
16	270.5	45.1	104	4	US-08-626-288-2
17	270.5	45.1	104	4	US-09-095-429-2
18	270.5	45.1	105	3	US-08-875-811-39
19	270.5	45.1	355	3	US-08-875-811-41
20	268.5	44.8	104	3	US-08-875-811-51
21	268.5	44.8	104	3	US-08-875-811-51
22	268.5	44.8	104	4	US-09-071-672-1
23	268.5	44.8	104	4	US-08-986-119-1
24	268.5	44.8	106	3	US-08-875-811-28
25	268.5	44.8	107	3	US-08-875-811-30
26	268.5	44.8	112	3	US-08-875-811-32
27	268.5	44.8	251	3	US-08-875-811-59

28	268.5	44.8	254	3	US-08-875-811-61	Sequence 61, Appl
29	268.5	44.8	355	3	US-08-875-811-49	Sequence 49, Appl
30	268.5	44.8	355	3	US-08-875-811-57	Sequence 57, Appl
31	268.5	44.8	355	3	US-08-875-811-64	Sequence 64, Appl
32	268.5	44.8	366	3	US-08-875-811-55	Sequence 55, Appl
33	263.5	43.9	105	3	US-08-875-811-24	Sequence 24, Appl
34	263.5	43.9	105	3	US-08-875-811-26	Sequence 26, Appl
35	259.5	43.2	358	3	US-08-875-811-45	Sequence 45, Appl
36	259.5	43.2	365	3	US-08-875-811-53	Sequence 53, Appl
37	245.5	40.9	107	3	US-08-875-811-20	Sequence 20, Appl
38	235.5	39.2	111	3	US-08-875-811-22	Sequence 22, Appl
39	232	38.7	114	3	US-09-223-118-3	Sequence 47, Appl
40	223.5	37.2	360	3	US-08-875-811-47	Sequence 3, Appl
41	223	37.2	114	3	US-09-223-118-2	Sequence 2, Appl
42	222	37.0	114	3	US-09-223-118-1	Sequence 1, Appl
43	221	36.8	114	3	US-09-223-118-4	Sequence 4, Appl
44	202	33.7	83	3	US-08-875-811-2	Sequence 2, Appl
45	202	33.7	83	4	US-09-071-672-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

Sat May 8 17:57:17 2004

PA (ALFA-) ALFACELL CORP.
XX
PI Saxena SK;
XX
DR WPI; 2001-167808/17.
XX
PT New nucleic acids encoding a ribonuclease (Knae), useful for the precise
PT targeting of Knae to a predetermined cell receptor.
XX
XX Claim 2; Col 5-6; 7pp; English.
XX
XX The present sequence represents a modified frog ribonuclease protein
CC (ranpirnase) (RNase). The synthetic ribonuclease comprises a cysteine
CC which facilitates the chemical linking of a targeting molecule by the
CC single reactive sulphydryl group. The specification describes a method
CC for the production of ranpirnase using DNA technology instead of
CC processing biological material. The re-engineering of the protein
CC molecule allows easier attachment to a targeting molecule thereby making
CC it possible for the ribonuclease to be delivered to a particular cell
CC receptor where it might be most effective
XX
SQ Sequence 104 AA;
Query Match 45.6%; Score 273.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 5.5e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFIISATTVKAICTGVI-NLN 58
Db 1 QDWLTFQKHITNTDRDVCNLLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 104
Search completed: May 7, 2004, 21:38:29
Job time : 47.9224 secs

PA Rana pipiens.
XX
PN WO9738112-A1.
XX
PD 16-OCT-1997.
XX
PF 04-APR-1997; 97WO-US005675.
XX
PR 04-APR-1996; 96US-00625288.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Youle RJ, Vasandani VM, Wu Y, Boix E, Ardelt W;
XX
DR WPI; 1997-512725/47.
XX
XX Recombinant Onc protein with glutamine residue at position 1 - useful as
PT antitumour and antiviral agent, also as cell culture selection agent.
PT
XX Claim 1; Page 28; 35pp; English.
XX
XX This sequence represents a recombinant Onc protein comprising a 104 amino
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating
CC pancreatic cancer) and inhibitor of human immunodeficiency virus type-1
CC replication. It can be used therapeutically or as a cell-culture
CC selection agent, e.g. to identify gene therapy compositions able to
CC inhibit tumour growth
XX
SQ Sequence 104 AA;
Query Match 45.6%; Score 273.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 5.5e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFIISATTVKAICTGVI-NLN 58
Db 1 QDWLTFQKHITNTDRDVCNLLSTNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
Db 57 VLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVCVCENQAPVHFVGVGSC 104

RESULT 15
AAB31667
ID AAB31667 standard; protein; 104 AA.
XX
AC AAB31667;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a modified frog ribonuclease protein.
XX
KW Frog; ribonuclease; ranpirnase; RNase.
XX
OS Synthetic.
OS Rana pipiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 23
FT Misc-difference 72 /note= "wild type Met changed to Leu"
FT Misc-difference 72 /note= "wild type Ser changed to Cys"
XX
XX US6175003-B1.
XX
PN 16-JAN-2001.
PD
XX 10-SEP-1999; 99US-00394268.
XX
XX 10-SEP-1999; 99US-00394268.
XX

KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.

OS Rana pipiens.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Met not found in wild type RaPLR1"

PN WO9950398-A2.
 XX
 XX
 PD 07-OCT-1999.
 XX
 XX
 PF 26-MAR-1999; 99WO-US006641.
 XX
 XX
 PR 27-MAR-1998; 98US-0079751P.
 XX
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Rybak SM, Newton DL;
 XX
 XX
 DR WPI; 1999-610847/52.
 DR N-PSDB; AAZ08126.
 XX

XX
 FT New recombinant ribonucleases, used for killing target cells, e.g. for
 FT treating cancers, viral infections or autoimmune diseases.
 XX

PS Claim 34; Page 57; 71pp; English.

XX
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1. Carboxy terminal end of recombinant
 CC RaPLR1 has a covalently bound ligand binding moiety, which can be a LL2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases

XX Sequence 105 AA;

SQ
 Query Match 46.2%; Score 277.5; DB 2; Length 105;
 Best Local Similarity 48.6%; Pred. No. 2e-23;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKATCGVI-NLN 58
 Db 2 QDWLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIATSKN 57
 QY 59 VLSTRFQNLCTRTSITPRPCYSRSTETNYICVKENQYVPHFAGIGRC 109
 Db 58 VLTTSEFYLSDC---NVTSRPCKYKLKSTNTFCVTCENQAPVPHFVGVC 105

RESULT 13
 AAY28879
 ID AAY28879 standard; protein; 127 AA.

XX
 XX
 AC AAY28879;
 XX
 XX 25-JAN-2000 (first entry)
 DT
 XX Rana pipiens Clone Salb ribonuclease.

XX Rana pipiens ribonuclease Clone Salb; RaPLR1; covalently bound; RNase;
 KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
 KW Kaposi's Sarcoma; human chorionic gonadotropin; hCG; cancer;
 KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

KW autoimmune disease.

XX Rana pipiens.

OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..23
 FT /label= Signal peptide
 FT /note= "Putative"
 FT 24..127
 FT Protein
 FT /label= Rana pipiens_Clone_Salb_ribonuclease

PN WO9950398-A2.

XX

PD 07-OCT-1999.

XX

PF 26-MAR-1999; 99WO-US006641.

XX

PR 27-MAR-1998; 98US-0079751P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Rybak SM, Newton DL;

XX

DR WPI; 1999-610847/52.

DR N-PSDB; AAZ08136.

XX

FT New recombinant ribonucleases, used for killing target cells, e.g. for

FT treating cancers, viral infections or autoimmune diseases.

XX

PS Disclosure; Page 69; 71pp; English.

XX

CC The present sequence is a Rana pipiens Clone Salb ribonuclease (RaPLR1).

CC It is encoded by Clone Salb cDNA obtained from Rana pipiens liver mRNA

CC library. It exhibits differences with Onconase (STM) at amino acid

CC residues 11, 20, 85 and 103. Carboxy terminal end of RaPLR1 has a

CC covalently bound ligand binding moiety, which can be a LL2 antibody

CC directed against CD22 on cancerous B cells or human chorionic

CC gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases

XX

SQ Sequence 127 AA;

Query Match 46.2%; Score 277.5; DB 2; Length 127;
 Best Local Similarity 48.6%; Pred. No. 2.5e-23;
 Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHIINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKATCGVI-NLN 58
 Db 24 QDWLTFQKHLNTRDVCNIMSTNLF---HCKDKNTFIYSRPPVKAICKGIATSKN 79
 QY 59 VLSTRFQNLCTRTSITPRPCYSRSTETNYICVKENQYVPHFAGIGRC 109
 Db 80 VLTTSEFYLSDC---NVTSRPCKYKLKSTNTFCVTCENQAPVPHFVGVC 127

RESULT 14
 AAW30301
 ID AAW30301 standard; protein; 104 AA.

XX
 XX AAW30301;
 XX
 XX 09-JUN-1998 (first entry)
 DT
 XX Recombinant onc protein.
 DE
 XX Onc; onconase; ribonuclease; frog; antitumor; pancreatic cancer;
 KW human immunodeficiency virus type-1; HIV1; replication.
 XX

ID AAY28869 standard; protein; 105 AA.
 XX
 AC AAY28869;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met(-1) RaPLR1 Met23Leu-(His)6 protein.
 XX
 KW Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RaPLR1;
 XX CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; frog; autoimmune disease.
 XX
 OS Rana pipiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 XX
 FT Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT
 FT Misc-difference 24 /note= "Wild type Met replaced with Leu"
 FT
 XX
 XX WO9950398-A2.
 XX
 XX 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US006641.
 XX
 XX 27-MAR-1998; 98US-0079751P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rybak SM, Newton DL;
 XX
 XX WPI; 1999-610847/52.
 DR
 DR N-PSDB; AAZ08127.
 XX
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX
 XX Claim 4; Page 59; 71pp; English.
 XX
 XX The present sequence is a recombinant Rana pipiens ribonuclease protein
 XX (RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
 XX Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand
 XX binding moiety, which can be a LL2 antibody directed against CD22 on
 XX cancerous B cells or human chorionic gonadotropin (hCG) effective
 XX against Kaposi's sarcoma cells. Recombinant ribonucleases can be
 XX expressed in bacteria without an N-terminal methionine due to the
 XX presence of a signal peptide that is cleaved by bacteria. The soluble
 XX expression of ribonuclease allows the proteins to be fused in-frame with
 XX ligand binding moieties to form cytotoxic fusion proteins. They can be
 XX used for treatment of cancer and autoimmune diseases
 XX
 XX Sequence 105 AA;
 SQ
 Query Match 46.6%; Score 279.5; DB 2; Length 105;
 Best Local Similarity 49.5%; Pred. No. 1.2e-23;
 Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
 DB 2 QDWLTFQKHLNTRDVCNNILNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 57
 QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNIVCKENCQYPVHFAGIGRC 109
 DB 58 VLITSEFYLSDC---NVTSRPCYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
 RESULT 11

AAY28865
 ID AAY28865 standard; protein; 104 AA.
 XX
 AC AAY28865;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Rana pipiens liver ribonuclease (RaPLR1).
 XX
 KW Rana pipiens liver ribonuclease; RaPLR1; covalently bound; LL2 antibody;
 XX ligand binding moiety; CD22; cancerous B cell; Kaposi's sarcoma; frog;
 KW human chorionic gonadotropin; hCG; recombinant ribonuclease; RNase;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX
 OS Rana pipiens.
 XX
 PN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US006641.
 XX
 XX 27-MAR-1998; 98US-0079751P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Rybak SM, Newton DL;
 XX
 XX WPI; 1999-610847/52.
 DR
 DR N-PSDB; AAZ08124.
 XX
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX
 XX Claim 1; Page 55; 71pp; English.
 XX
 XX The present sequence is Rana pipiens liver ribonuclease (RaPLR1) protein.
 XX Carboxy terminal end of RaPLR1 has a covalently bound ligand binding
 XX moiety, which can be a LL2 antibody directed against CD22 on cancerous B
 XX cells or human chorionic gonadotropin (hCG) effective against Kaposi's
 XX Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 XX without an N-terminal methionine due to the presence of a signal peptide
 XX that is cleaved by bacteria. The soluble expression of ribonuclease
 XX allows the proteins to be fused in-frame with ligand binding moieties to
 XX form cytotoxic fusion proteins. They can be used for treatment of cancer
 XX and autoimmune diseases
 XX
 XX Sequence 104 AA;
 SQ
 Query Match 46.2%; Score 277.5; DB 2; Length 104;
 Best Local Similarity 48.6%; Pred. No. 1.9e-23;
 Matches 54; Conservative 16; Mismatches 33; Indels 9; Gaps 4;
 QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
 DB 1 QDWLTFQKHLNTRDVCNNILNLF---HCKDKNTFIYSRPEPVKAICKGIASKN 56
 QY 59 VLSTTRFQNTCTRTSITPRCPYSSRTETNIVCKENCQYPVHFAGIGRC 109
 DB 57 VLITSEFYLSDC---NVTSRPCYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
 RESULT 12
 AAY28867
 ID AAY28867 standard; protein; 105 AA.
 XX
 AC AAY28867;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met(-1) RaPLR1.
 XX
 KW Recombinant Met(-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;

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CC (Rana catesbeiana) lectin used to describe the method of the invention
XX
SQ Sequence 111 AA;

Query Match          97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 6.5e-58;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 ENWATFOQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 60 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8
AAW06544
ID ID AAW06544 standard; protein; 104 AA.
XX
AC AAW06544;
XX
DT 22-AUG-1997 (first entry)
XX
DE Antitumour protein from Rana pipiens oocytes.
XX
KW Tumour; chemotherapy; radiotherapy; frog.
XX
OS Rana pipiens.
XX
PN WO9639428-A1.
XX
PD 12-DEC-1996.
XX
PF 03-JUN-1996; 96WO-US008304.
XX
PR 06-JUN-1995; 95US-00467955.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Ardelt WJ;
XX
PS WPI; 1997-043063/04.
XX
PT Antitumour proteins from Rana pipiens oocyte(s) - have fewer
PT disadvantages than chemotherapy, surgery and radiotherapy.
XX
PS Claim 8; Page 28; 45pp; English.
XX
CC The present sequence is a specifically claimed example of an antitumour
CC protein from the generic protein in AAW18224, with the molecular weight
CC 12000. This is one of two preferred proteins (the other in AAW06543) that
CC have been isolated from Rana pipiens oocytes. Both proteins have a
CC blocked amino terminal group and are essentially free of carbohydrates.
CC The proteins are used to treat tumours. Use of the peptides has fewer
CC disadvantages than chemotherapy, radiotherapy and surgery in the
CC treatment of tumours
XX
SQ Sequence 104 AA;

Query Match          46.8%; Score 280.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 8.8e-24;
Matches 54; Conservative 17; Mismatches 31; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 58
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EDWLTFOQKHVINTRDVDNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 109
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 57 VLTTFSEFYLSDC---NVTSRPCQKYLKSKTNTFCVTCENQAPVHFVGVGRC 104
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 9
AAW28866
ID ID AAY28866 standard; protein; 104 AA.
XX
AC AAY28866;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaPLR1 Met23Leu amino acid sequence.
XX
KW Recombinant Rana pipiens ribonuclease; RaPLR1 Met23Leu; covalently bound;
KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW autoimmune disease.
XX
OS Rana pipiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08125.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 34; Page 56; 71pp; English.
XX
CC The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
CC protein with Met23Leu. Carboxy terminal end of recombinant RaPLR1 has a
CC covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases
XX
SQ Sequence 104 AA;

Query Match          46.6%; Score 279.5; DB 2; Length 104;
Best Local Similarity 49.5%; Pred. No. 1.1e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 58
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QDWLTFOQKHVINTRDVDNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 59 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 109
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 57 VLTTFSEFYLSDC---NVTSRPCQKYLKSKTNTFCVTCENQAPVHFVGVGHC 104
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RESULT 10
AAY28869

Sat May 8 17:57:17 2004

SQ Sequence 110 AA;

Query Match 98.5%; Score 591; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 7.1e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQKHIIINTPIICNTILDNNIIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61
DB 2 NWATFQKHIIINTPIICNTILDNNIIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61

QY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110
DB 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110

RESULT 6
AAY28878
ID AAY28878 standard; protein; 111 AA.
XX AC AAY28878;
XX DT 25-JAN-2000 (first entry)
XX DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW CD22; RNase; autoimmune disease.
XX OS Rana catesbeiana.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
XX WO9950398-A2.
XX PD 07-OCT-1999.
XX PF 26-MAR-1999; 99WO-US006641.
XX PF 27-MAR-1998; 98US-0079751P.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL;
XX DR WPI; 1999-610847/52.
XX DR N-PSDB; AA208135.
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX PT treating cancers, viral infections or autoimmune diseases.
XX PS Claim 22; Page 68; 71pp; English.
XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease
CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotropin (hCG) effective against Kaposi's sarcoma cells.
CC Recombinant ribonucleases can be expressed in bacteria without an N-
CC terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
XX autoimmune diseases
XX SQ Sequence 111 AA;

Query Match 98.5%; Score 591; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 7.1e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWATFQKHIIINTPIICNTILDNNIIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 61
DB 3 NWATFQKHIIINTPIICNTILDNNIIYVGGQCKRVNTFIISATTVKATCTGVINLVLS 62

QY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRCP 111

RESULT 7
AAY33321
ID AAY33321 standard; protein; 111 AA.
XX AC AAY33321;
XX DT 29-NOV-1999 (first entry)
XX DE Frog lectin protein fragment.
XX KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX OS Rana catesbeiana.
XX OS US955073-A.
XX PD 21-SEP-1999.
XX PF 09-JUL-1997; 97US-00891848.
XX PR 20-APR-1990; 90US-00510696.
XX PR 22-OCT-1991; 91US-0079195.
XX PR 04-FEB-1993; 93US-00014082.
XX PR 22-SEP-1993; 93US-00125462.
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX DR WPI; 1999-560488/47.
XX PT Recombinantly fused pancreatic RNase-targeting proteins useful for
XX PT treating tumors, infections, immune or autoimmune disorders and as a
XX PT contraceptive.
XX PS Example 3; Fig 19; 47pp; English.
XX CC This invention describes a novel nucleic acid construct comprising
CC sequences encoding functional pancreatic RNase and a second protein
CC (preferably the light and heavy chains of an antibody) which binds a
CC specific cell surface marker on a target cell and functions as a
CC cytotoxic agent. The products can be used for selectively killing cells
CC expressing a specific surface marker. They can be used for treating
CC tumors or infected cells (e.g. cells infected by viruses (especially
CC latent or chronic virus infections, such as human immunodeficiency virus
CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
CC II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster, and
CC cytomegalovirus) and cells infected with parasites (such as the malaria
CC parasite)). They can also be used for treating immune dysfunctional cells
CC in immune and autoimmune diseases. Additionally, they may be used as
CC contraceptives. Finally they can also be used for cell separation in
CC vitro by selectively killing unwanted types of cells (e.g. in bone
CC marrow) prior to transplantation into a patient undergoing marrow
CC ablation by radiation or for killing leukemia cells or T-cells that would
CC cause graft-versus-host disease. This sequence represents a bullfrog

CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX
SQ Sequence 110 AA;

Query Match 99.3%; Score 596; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.9e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60
QY 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4
AA28873
ID AAY28873 standard; protein; 111 AA.
XX
AC AAY28873;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met (-1) RaCOR1.

XX
KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
FT XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
DR N-PSDB; AA208131.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
FT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 63; 71pp; English.

XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX
SQ Sequence 111 AA;

Query Match 99.3%; Score 596; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.9e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 60
Db 2 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVAICTGVINLNL 61
QY 61 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 STTRFQMLTCTRTSITPRPCVSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 5
AA28877
ID AAY28877 standard; protein; 110 AA.
XX
AC AAY28877;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaCOR1 Gln1Ser amino acid sequence.

XX
KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.

Key Location/Qualifiers
FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
FT XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US006641.
XX
PR 27-MAR-1998; 98US-0079751P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PI Rybak SM, Newton DL;
XX
DR WPI; 1999-610847/52.
XX
DR N-PSDB; AA208134.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
FT treating cancers, viral infections or autoimmune diseases.
XX
PS Claim 22; Page 67; 71pp; English.

XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC Recombinant ribonucleases can be expressed in bacteria without an N-
CC terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases
XX

CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases
 XX Sequence 110 AA:

Query Match 100.0%; Score 600; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.8e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60
 DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110

RESULT 2
 AAY28876
 ID AAY28876 standard; protein; 111 AA.

AC AAY28876;
 DT 25-JAN-2000 (first entry)
 DE Recombinant Met (-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
 KW Met (-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.

OS Rana catesbeiana.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

PN WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rybak SM, Newton DL;
 XX WPI: 1999-610847/52.
 DR N-PSDB; AAZ08133.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 66; 71pp; English.

CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a (His)6
 CC tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant RaCOR1
 CC has a covalently bound ligand binding moiety, which can be a LL2 antibody
 CC directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases
 XX Sequence 111 AA:

Query Match 100.0%; Score 600; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.8e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 60
 DB 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLVL 61
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 110
 DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVHFAGIGRCP 111

RESULT 3
 AAY28872
 ID AAY28872 standard; protein; 110 AA.

AC AAY28872;
 DT 25-JAN-2000 (first entry)
 DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
 KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.

OS Rana catesbeiana.
 OS Synthetic.
 PN WO9950398-A2.
 XX 07-OCT-1999.
 XX 26-MAR-1999; 99WO-US006641.
 XX 27-MAR-1998; 98US-0079751P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Rybak SM, Newton DL;
 XX WPI: 1999-610847/52.
 DR N-PSDB; AAZ08130.
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 XX treating cancers, viral infections or autoimmune diseases.
 XX Claim 22; Page 62; 71pp; English.

CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:25:55 ; Search time 46.9224 Seconds
(without alignments)
662.376 Million cell updates/sec

Title: US-09-961-400-19

Perfect score: 600

Sequence: 1 QNWAFFQKHINTPIICNT.....ICVKENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: A Geneseqp29Jan04.*
2: Geneseqp1980s.*
3: Geneseqp1990s.*
4: Geneseqp2000s.*
5: Geneseqp2001s.*
6: Geneseqp2002s.*
7: Geneseqp2003as.*
8: Geneseqp2003bs.*
9: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	600	100.0	110	2	AAY28874
2	600	100.0	111	2	AAY28876
3	596	99.3	110	2	AAY28872
4	596	99.3	111	2	AAY28873
5	591	98.5	110	2	AAY28877
6	591	98.5	111	2	AAY28878
7	582.5	97.1	111	2	AAY28879
8	280.5	46.8	104	2	AAY28880
9	279.5	46.6	104	2	AAY28881
10	279.5	46.6	105	2	AAY28882
11	277.5	46.2	104	2	AAY28883
12	277.5	46.2	105	2	AAY28884
13	277.5	46.2	127	2	AAY28885
14	273.5	45.6	104	2	AAY28886
15	273.5	45.6	104	2	AAY28887
16	273.5	45.6	104	2	AAY28888
17	273.5	45.6	104	2	AAY28889
18	273.5	45.6	104	2	AAY28890
19	273.5	45.6	105	2	AAY28891
20	273.5	45.6	379	2	AAY28892
21	272.5	45.4	104	2	AAY28893
22	272.5	45.4	104	2	AAY28894
23	272.5	45.4	105	2	AAY28895
24	270.5	45.1	104	2	AAY28896
25	270.5	45.1	104	2	AAY28897

26	270.5	45.1	104	2	AAW00736	AAW00736 Protein d
27	270.5	45.1	104	2	AAW14065	AAW14065 Onconase
28	270.5	45.1	104	2	AAW06543	AAW06543 Anticimou
29	270.5	45.1	104	2	AAW88233	AAW88233 Rana pipi
30	270.5	45.1	104	2	AAW33322	AAW33322 Frog onco
31	270.5	45.1	105	2	AAW35123	AAW35123 R. pipien
32	270.5	45.1	355	2	AAW35125	AAW35125 R. pipien
33	270.5	45.1	358	2	AAW35130	AAW35130 R. pipien
34	268.5	44.8	106	2	AAW35122	AAW35122 R. pipien
35	268.5	44.8	107	2	AAW35117	AAW35117 R. pipien
36	268.5	44.8	112	2	AAW35118	AAW35118 R. pipien
37	268.5	44.8	251	2	AAW35134	AAW35134 R. pipien
38	268.5	44.8	254	2	AAW35135	AAW35135 R. pipien
39	268.5	44.8	355	2	AAW35133	AAW35133 R. pipien
40	268.5	44.8	355	2	AAW35129	AAW35129 R. pipien
41	268.5	44.8	366	2	AAW35132	AAW35132 R. pipien
42	263.5	43.9	104	2	AAW18224	AAW18224 Anticimou
43	263.5	43.9	105	2	AAW35115	AAW35115 R. pipien
44	263.5	43.9	105	2	AAW35116	AAW35116 R. pipien
45	259.5	43.2	358	2	AAW35127	AAW35127 R. pipien

ALIGNMENTS

RESULT 1

RAY28874	ID	RAY28874	standard; protein; 110 AA.
XX	AC	RAY28874;	
XX	DT	25-JAN-2000	(first entry)
XX	DE	Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.	
XX	KW	Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound; cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog; RNase; autoimmune disease.	
XX	OS	Rana catesbeiana.	
XX	OS	Synthetic.	
XX	Key	Location/Qualifiers	
FT	Misc-difference 22	/note= "Wild type Met replaced with Leu"	
FT	Misc-difference 57	/note= "Wild type Met replaced with Leu"	
FT	XX	WO9950398-A2.	
XX	PD	07-OCT-1999.	
XX	PF	26-MAR-1999;	99WO-US006641.
XX	PR	27-MAR-1998;	98US-0079751P.
XX	XX	(USSH)	US DEPT HEALTH & HUMAN SERVICES.
XX	PI	Rybak SM,	Newton DL;
XX	DR	WPI; 1999-610847/52.	
XX	DR	N-PSDB; AA208132.	
XX	XX	New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases.	
XX	XX	Claim 22; Page 64; 71pp; English.	
XX	CC	The present sequence is a recombinant Rana catesbeiana oocyte ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal end of recombinant RaCOR1 has a covalently bound ligand binding moiety,	

```

RA Beintema J.J.;
RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
RL Gene 212:259-268(1998).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
-----
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-----
CC EMBL; Y11670; CAAV2368.1; -.
CC HSSP; P00656; ISRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea_1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR SMART; PD000535; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SMO0092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT ACT SITE 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC...) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 151 AA; E95F3757FFC5B233 CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 151;
Best Local Similarity 30.6%; Pred. No. 8.5e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

Qy 5 ATPQKH-----INTPLCNTMDNNIYVGQCQRVNTFISSATTVKICTGVNM 58
|:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 6 AKFRQHMDAGSGSSGNSNYCNQMKKR-RMTHGRCKPVNTFVHESLDVAVCS---QK 61
|:::| |:::| |:::| |:::| |:::| |:::| |:::|
Qy 59 NVL-----STTRFLQNLTCRTSITPRP-CPYSSRSETETNICVKE-NQY-PVHEFA 105
|:::| |:::| |:::| |:::| |:::| |:::| |:::|
Db 62 NITCKNGPNCYQSINMTWTDRETGSCKYPNCAYKTSQXKYITVACEGNPVVPVHF 121
|:::| |:::| |:::| |:::| |:::| |:::| |:::|
Qy 106 G 106
Db 122 G 122

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Sat May 8 17:57:16 2004

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OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]_SEQUENCE.
RP SEQUENCE.
RC TISSUE=Wilk, and Serum; PubMed=9256695;
RX MEDLINE=97409980; PubMed=9256695;
RA Strödom D.J., Bond M.D., Vallee B.L.;
RT "An angiogenic protein from bovine serum and milk -- purification and
RT primary structure of angiogenin-2";
RL Eur J Biochem. 247:535-544(1997).
CC -!- FUNCTION: Binds tightly to placental ribonuclease inhibitor and
CC has very low ribonuclease activity. Has potent angiogenic
CC activity. Angiogenin induces vascularization of normal and
CC malignant tissues. Abolishes protein synthesis by specifically
CC hydrolyzing cellular tRNAs.
CC -!- TISSUE SPECIFICITY: Serum and milk.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC HSSP; P10152; IAGI.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Glycoprotein;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 39 39 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.
FT DISULFID 25 80
FT DISULFID 38 91
FT DISULFID 56 106
FT CARBOHYD 33 33 N-LINKED (GLCNAC... )
SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 123;
Best Local Similarity 30.6%; Pred. No. 6.9e-07;
Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;

Oy 7 PQKHINTPT-----ICNTMDNNIYVGGCKRVNTFISSATTVKAIK---TGVINM 58
Db 8 FLRKHDPSPGCHDDRYCNTMWER--NTPKCKDNTNFIHGNSDDIRAVCDRNGEYR 65
Oy 59 NVLSTTR--FQNLCTRTSITPR-PCPYSSRTETNYICVKENQYVPH 103
Db 66 NGLRERSPPFQVTTCTHRGSRPPCYRAFRANRVIVIRCDRGFFIH 113

RESULT 14
RNBR GIRCA STANDARD; PRT; 141 AA.
AC Q29542; Q29533;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ribonuclease, brain (BC 3.1.27.-) (BRB).
GN BRN.
OS Giraffa camelopardalis (Giraffe).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Giraffoidea;
OC Giraffidae; Giraffa.
OX NCBI_TaxID=9894;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=96139017; PubMed=8587129;
RX Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
RA Vento M.T., Furia A.;
RA "Molecular evolution of genes encoding ribonucleases in ruminant
RT species.";
RL J. Mol. Evol. 41:850-858(1995).

[2]
RN SEQUENCE OF 31-114 FROM N.A.
RP MEDLINE=93367815; PubMed=8360916;
RX Breukelman H.J., Beintema J.J., Confalone E., Costanzo C., Sasso M.P.,
RA Carsana A., Palmieri M., Furia A.;
RT "Sequences related to the ox pancreatic ribonuclease coding region in
RT the genomic DNA of mammalian species.";
RL J. Mol. Evol. 37:29-35(1993).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC -----
CC EMBL; S81743; AAB36137.1; -
CC EMBL; S65126; AAB27931.1; -
CC HSSP; P00656; 2RNS.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNaseA; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Glycoprotein.
KW ACT_SITE 41 41 BY SIMILARITY.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC... ) (BY SIMILARITY).
FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 141 AA; 15592 MW; 73745EFE9079591F CRC64;

Query Match 21.0%; Score 127.5; DB 1; Length 141;
Best Local Similarity 30.6%; Pred. No. 7.9e-07;
Matches 37; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

Oy 5 ATFOQKH-----INTPLICNTMDNNIYVGGCKRVNTFISSATTVKAICTGVINM 58
Db 6 AKFRQHMDSGSSSSNSNYCNQMKR-RMTHRCXFPVNTFVHESLADVKAVCS---QK 61
Oy 59 NVL-----STTRFQLNCTRTSITPR-PCPYSSRTETNYICVKE-NQY-PVHFA 105
Db 62 NITCKGQPCYQSNSTMTNITDCTETGSSKYPNCAYKTSQKQYITVACEGNPYVPHED 121
Oy 106 G 106
Db 122 G 122

RESULT 15
RNBR AXIPR STANDARD; PRT; 151 AA.
AC P87350;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, brain (BC 3.1.27.-) (BRB).
GN BRN.
OS Axis porcinus (Hog deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea;
OC Cervidae; Cervinae; Axis.
OX NCBI_TaxID=57737;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=98278842; PubMed=9611269;
RX Breukelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
RA

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SQ SEQUENCE      124 AA;  13804 MW;   0AC28CDE14111845 CRC64;
Query Match          21.8%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 2e-07;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FQQKHI-----INTPIICTIMDNNNIYIVGGCKRVNTFISSATVKAICGV-INNM 59
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 8 FQRQHMDPSSSSNSSNYCNLMMSRR-NWTQGRCKPVNTFVHESLADVOAVCSQINVC 66
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 60 VLSTTRFQLNT-----CTRSITPRP-CPXSSRTETNYICVKENQ--YPVHF 104
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 67 NGQTNCYQSNTMHTTDCRGTGSSKYPCAYKASOEQRKHIIIVACEGNPPVPVHF 120
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 11
RNP_IGUIG
ID_RNP_IGUIG STANDARD; PRT; 119 AA.
AC PF0287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (SC 3.1.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
RT ribonuclease."
RL Eur. J. Biochem. 219:641-646(1994).
CC -! CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! TISSUE SPECIFICITY: Pancreas.
CC -! SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; S4111; S4111.
DR HSP; P00656; IL5Q.
DR InterPro; IPRO01427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase Pg; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Pyrididone carboxylic acid.
FT MOD_RES 1 1
FT DISULFID 25 80
FT FT 1 BY SIMILARITY.
FT DISULFID 39 91
FT FT 1 BY SIMILARITY.
FT DISULFID 57 106
FT FT 1 BY SIMILARITY.
FT ACT SITE 10 10
FT FT 1 BY SIMILARITY.
FT ACT SITE 40 40
FT FT 1 BY SIMILARITY.
FT ACT SITE 113 113
FT FT 1 BY SIMILARITY.
SQ SEQUENCE      119 AA;  13324 MW;   6072FB5B7B15BD5A CRC64;
Query Match          21.7%; Score 131.5; DB 1; Length 119;
Best Local Similarity 30.4%; Pred. No. 2.5e-07;
Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 2 QNWATFOOKHI-----INTPIICTIMDNNNIYIVGGCKRVNTFISSATVKAIC-- 52
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 QDWSSFQNKHIDYDTPETGASNPNVAYCDLMWQRR-NLNPTKCKTRNTFVASPSIEIQOVCS 59
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 53 --TGVINNVLTSTRFQLNTCTRTSIT-PRCPYSRRTETNYICVKENQYVPVHF 104
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 60 GGTHYEDNLVDNSFSDLTDCKNVGGTAPSSCKYNGTPTGTRIRIACENNQPVHF 114
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 12

```

16-OCT-2001 (Rel. 40, Last annotation update)
 Ribonuclease, Brain precursor (EC 3.1.27.-) (BRB).
 BRN.
 OS Bos taurus (Bovine).
 OOS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 OX [1]
 RP SEQUENCE FROM N.A.
 RP MEDLINE=92093604; PubMed=1754384;
 RX Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
 RX Viola M., Palmieri M., Russo E., Furia A.;
 RA "Molecular cloning of the gene encoding the bovine brain ribonuclease
 RT and its expression in different regions of the brain.";
 RT Nucleic Acids Res. 19:6469-6474 (1991).
 RL [2]
 RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.
 RP TISSUE=Brain;
 RC MEDLINE=89214015; PubMed=3243767;
 RX Watanabe H., Kato H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
 RA Ohgi K., Irie M.;
 RA "Primary structure of a ribonuclease from bovine brain.";
 RT J. Biochem. 104:939-945 (1988).
 RL [3]
 RP SEQUENCE OF 27-167 FROM N.A.
 RP MEDLINE=96139017; PubMed=8587129;
 RX Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
 RA Vento M.T., Furia A.;
 RA "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species.";
 RT J. Mol. Evol. 41:850-858 (1995).
 RL [4]
 RP SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC -----
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 CC -----
 CC EMBL; X59767; CAA42439.1; -;
 CC EMBL; S81744; AAB36138.1; -;
 CC PIR; S20066; S20066.
 CC HSP; P00656; 2RNS.
 CC GlycoSuiteDB; P39873; -;
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; rnasea; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNase PC; 1.
 CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW Hydrolase, Nuclease, Endonuclease, Glycoprotein, Signal.
 FT SIGNAL
 FT CHAIN
 FT 1 26 RIBONUCLEASE, BRAIN.
 FT 27 167 BY SIMILARITY.
 FT ACT SITE 38 38 BY SIMILARITY.
 FT ACT SITE 67 67 BY SIMILARITY.
 FT ACT SITE 145 145 BY SIMILARITY.
 FT DISULFID 52 110 BY SIMILARITY.
 FT DISULFID 66 121 BY SIMILARITY.
 FT DISULFID 84 136 BY SIMILARITY.
 FT DISULFID 91 98 BY SIMILARITY.
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. .).
 FT /FTID=CAR 000005.
 FT CARBOHYD 155 155 O-LINKED.
 FT CARBOHYD 159 159 O-LINKED.
 FT CONFLICT 155 155 T -> S (IN REF. 2).
 FT SEQUENCE 167 AA; 18450 MW; 681CAAG3CC2FC459 CRC64;
 SQ
 Query Match 22.0%; Score 133.5; DB 1; Length 167;
 Best Local Similarity 31.4%;
 Pred. No. 2.1e-07;
 Pred. No. 1.1e-07;

Matches	38;	Conservative	17;	Mismatches	43;	Indels	23;	Gaps	7;
QY	5	ATFOQKHI-----INTPLICNTIMNNIYVGQCKRVNTFIISATTVKAICTGVINN	58						
DB	32	AKFRQHMDSGSSSSSNFYCNQMKKRR-RWTHGRCKPVNTFVHESLDDVKAVCS---OK	87						
QY	59	NVL-----SITTFQLNTCTRTSTTPR-CPYSSRTETNYICVKE-NQY-PVHFA	105						
DB	98	NITCKNGHCNCVQSKSTSIITDCRETGSKYPNCAYKTSQKQKIITVACEGPNYPVPVHFD	147						
QY	106	G 106							
DB	148	G 148							

RESULT 10	
RNP_PIG	STANDARD; PRT; 124 AA.
ID -RNP_PIG	
AC P00671;	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
DE	RNASE1 OR RNS1.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC	NCBI_Taxid=9823;
OX	[1]
RN	SEQUENCE.
RX	MEDLINE=70104197; PubMed=5460946;
RA	Jackson R.L., Hirs C.H.W.;
RA	"The primary structure of porcine pancreatic ribonuclease. II. The
RT	amino acid sequence of the reduced S-aminoethylated protein.";
RL	J. Biol. Chem. 245:637-653(1970).
RN	[2]
RN	REVISION TO 2.
PA	Wierenga R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
RT	"Affinity chromatography of porcine pancreatic ribonuclease and
RT	reinvestigation of the N-terminal amino acid sequence.";
RL	FEBS Lett. 31:181-185(1973).
RN	[3]
RN	DISULFIDE BONDS.
RP	MEDLINE=70104198; PubMed=4904878;
RX	Phelan J.J., Hirs C.H.W.;
RA	"The primary structure of porcine pancreatic ribonuclease. 3. The
RT	disulfide bonds.";
RL	J. Biol. Chem. 245:654-661(1970).
CC	-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC	with 2',3'-cyclic phosphate intermediates.
CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Pancreas.
CC	-!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR	PIR; A92071; NRPG.
DR	HSP; P00656; 1SRN.
DR	InterPro: IPR001427; RNaseA.
DR	PIfam: PF00074; rnaseA; 1.
DR	PRINTS; PR00794; RIBONUCLEASE.
DR	ProDom: PD000535; RNaseA; 1.
DR	SMART; SM00092; RNase Pg; 1.
DR	PROSITE; PS00127; RNASE PANCREATIC; 1.
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT	DISULFID 26 84
FT	DISULFID 40 95
FT	DISULFID 58 110
FT	DISULFID 65 72
FT	ACT_SITE 12 12
FT	ACT_SITE 41 41
FT	ACT_SITE 119 119
FT	CARBOHYD 21 21
FT	CARBOHYD 34 34
FT	CARBOHYD 76 76

BY SIMILARITY.	
BY SIMILARITY.	
BY SIMILARITY.	
N-LINKED (GLCNAC. .)	
N-LINKED (GLCNAC. .)	
N-LINKED (GLCNAC. .)	

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DR PIR; A00818; NRWHK.
DR HSP; P00656; LSRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 76 76 N-LINKED (GLUCNA... ) (30%).
SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 22.3%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 9.5e-08;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQKHII-----NTPILCNTMDNNIVIGSOCKRVNTFISSATTVKAICTGVNNV 60
Db 8 FQKHMDGNSPGNNPNCQMMRR-KWTGCKPVTNFVHSELDYKAVCS---QKNV 63
QY 61 I-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
Db 64 LCKNGRTNVCYNSMTHTDCRQSGSKYPNCAKYSQKEHIIIVACEGNYVPVHF 120

RESULT 8
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE Angiogenin precursor (EC 3.1.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Liver;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length

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RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
  angiogenins: discernment of functionally important residues and
  regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: May function as a tRNA-specific ribonuclease that binds
  to actin on the surface of endothelial cells; once bound,
  angiogenin is endocytosed and translocated to the nucleus, thereby
  promoting the endothelial invasiveness necessary for blood vessel
  formation. Angiogenin induces vascularization of normal and
  malignant tissues. Abolishes protein synthesis by specifically
  hydrolyzing cellular tRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC -----
DR EMBL; U22516; AAA91366.1; -.
DR EMBL; BC055355; AAH55355.1; -.
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:88022; Ang.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase P; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyroliadone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145 ANGIOENIN.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY
  SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query Match 22.3%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 1.1e-07;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFFIISATTVKAIC---TGVNNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 88
Db 63 CKDVTTFHGNKSNKKAICGANGSPYRNLRMSPFQVTTCKTGTGSPRPCCYRASAG 122
QY 89 TNYICVKEQYVPVHF 104
Db 123 FRHVVIACENGLPVHF 138

RESULT 9
RNER_BOVIN
ID RNER_BOVIN STANDARD; PRT; 167 AA.
AC P39873;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)

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T developmentally regulated genes when expressed in NIH 3T3
L fibroblasts.";
Mol. Cell. Biol. 17:1503-1512(1997)).
C -!- FUNCTION: Angiogenin induces vascularization of normal and
C malignant tissues. Abolishes protein synthesis by specifically
C hydrolyzing cellular tRNAs (By similarity).
C -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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C between the Swiss Institute of Bioinformatics and the EMBL outstation
C the European Bioinformatics Institute. There are no restrictions on its
C use by non-profit institutions as long as its content is in no way
C modified and this statement is not removed. Usage by and for commercial
C entities requires a license agreement (See http://www.isb-sib.ch/announce/
C or send an email to license@isb-sib.ch).

C EMBL; U72672; AAC05794.1; -;
R HSSP; P10152; IAGI.
R MGD; MGI:1201793; Ancl.
R InterPro; IPR001427; RNaseA.
R Pfam; PF00074; rnaseA; 1.
R PRINTS; PR00794; RIBONUCLEASE.
R ProDom; PD000535; RNaseA; 1.
R SMART; SMO0092; RNASE PC; 1.
R PROSITE; PS00127; RNASE PANCREATIC; 1.
R Hydrolase; Nuclease; Endonuclease; Angiogenesis;
K Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
F SIGNAL 1 24 POTENTIAL.
F CHAIN 25 145 ANGIOGENIN-3.
F MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID
(FY SIMILARITY).
F ACT_SITE 37 37 BY SIMILARITY.
F ACT_SITE 64 64 BY SIMILARITY.
F ACT_SITE 137 137 BY SIMILARITY.
F DISULFD 50 104 BY SIMILARITY.
F DISULFD 63 115 BY SIMILARITY.
F DISULFD 81 130 BY SIMILARITY.
Q SEQUENCE 145 AA; 16696 MW; DE9D3BC92FDD682C CRC64;
SQ
Query Match 25.5%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred.No.1e-09;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
QY 34 CKRVNFTFISSATTVKAIC-----TGVINNVLTSTRQLNTCTRTSTTPR-PCPYGSR 86
Db |||||::: :|||| |:::|||:::|::|:
63 KEVNTEFHDTKNNAIKACGGNGRPYG-V-NFSRFQTTCCKHGGSPRCPOYNAF 120
QY 87 TETNYIVCKENQYPVHF 104
Db : ||: |:|:|:
121 KDFRYIVTIACEDGWPHVF 138
RESULT 6
ANGR_MOUSE ID ANGR MOUSE STANDARD; PRT; 145 AA.
DT DT Q64438; AC
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
OS ANGRI.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.B., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RT protein gene and two pseudogenes.";
RT biochemistry 29:200-206(1995).

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RL J. Biochem. 106:729-735 (1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0085; JX0085.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.6%; Score 374; DB 1; Length 111;
Best Local Similarity 65.8%; Pred. No. 1.9e-33;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 59
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QNWAFFKEKHIRSTSSIDCITMDKAIYVGGCKERTNFIISDENVKICSGVSPDRK 60
QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ELSTTSFKLNTCTSDITPRPCPYHSPDNNKICVKCEKQLPVHFVGIGKC 111

RESULT 4
RN30_RANPI STANDARD; PRT; 104 AA.
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=1985896;
RA Ardel W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251 (1991).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosmann S.C., Johns K.L., Ardel W., Mikulski S.M., Shogen K.,
RA James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein:
a novel antitumor protein of Rana pipiens oocytes and early
embryos.";
RL Proteins 14:392-400 (1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94166079; PubMed=8120892;
RA Mosmann S.C., Ardel W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153 (1994).

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CC -1- FUNCTION: Basic protein with antiproliferative/cytotoxic activity
CC against several tumor cell lines in vitro, as well as antitumor
CC in vivo. It exhibits a ribonuclease-like activity against high
CC molecular weight ribosomal RNA.
CC -1- DEVELOPMENTAL STAGE: Early embryos (up to four blastomere stage).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PDB; 1ONC; 31-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75
FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 45.7%; Score 277.5; DB 1; Length 104;
Best Local Similarity 49.5%; Pred. No. 4.2e-23;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NMN 59
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 QDWLTFOKKHITNTRDVCNIMSTNLF----HCKKNFTIYRPFVKAICKGITASKN 56
QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:
57 VLTTSEFYLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

RESULT 5
ANG3_MOUSE STANDARD; PRT; 145 AA.
AC P97802;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE (EF-5).
GN ANG3 OR ANGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97184476; PubMed=9032278;
RA Fu X., Kamps M.P.;
RT "E2a-Fbx1 induces aberrant expression of tissue-specific and

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residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin. It is cytotoxic against several tumor cells.

-- SUBUNIT: Monomer.

-- SUBCELLULAR LOCATION: Secreted.

-- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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EMBL; AF039104; AAD10702.1; -.
DR DR
PIR; A27121; A27121.
DR DR
PDB; 1BC4; 28-OCT-98.
DR DR
PDB; 1M07; 21-JAN-03.
DR DR
InterPro; IPR001427; RNaseA.
DR DR
Pfam; PF00074; rnaaseA; 1.
DR DR
ProDom; PD000535; RNaseA; 1.
DR DR
SMART; SM00092; RNase_Pc; 1.
DR DR
PROSITE; PS00127; RNASE_PANCREATIC; 1.
DR DR
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Signal; Pyrrolidone carboxylic acid.
FT FT
FT SIGNAL 1 22
FT FT RIBONUCLEASE, OOCYTES.
FT FT
FT CHAIN 23 133
FT FT
FT MOD_RES 23 133
FT FT
FT ACT_SITE 32 32
FT FT
FT ACT_SITE 57 57
FT FT
FT ACT_SITE 125 125
FT FT
FT DISULFID 41 93
FT FT
FT DISULFID 56 103
FT FT
FT DISULFID 74 118
FT FT
FT DISULFID 115 132
FT FT
FT HELIX 25 32
FT FT
FT HELIX 41 45
FT FT
FT TURN 48 49
FT FT
FT STRAND 59 63
FT FT
FT HELIX 67 73
FT FT
FT TURN 74 74
FT FT
FT STRAND 79 84
FT FT
FT STRAND 90 95
FT FT
FT STRAND 105 110
FT FT
FT STRAND 114 119
FT FT
FT TURN 120 121
FT FT
FT STRAND 122 129
FT FT
FT SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;
SO

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Query Match	97.4%;	Score	591.5;	DB 1;	Length	133;
Best Local Similarity	99.1%;	Pred. No.	9.4e-57;			
Matches 110;	Conservative	0;	Mismatches	0;	Indels	1;
Gaps	1;					
2	QNWATFQQKHIIINTPII	-CNTIMDNNIYIVGGCKRVNTFI	ISSATTVKAICTGVINMNV	60		
23	QNWATFQQKHIIINTPII	NCNTIMDNNIYIVGGCKRVNTFI	ISSATTVKAICTGVINMNV	82		
61	LSTTRFQLNCTCETST	TPRCPYSSRTEIN YICVKENQYVHFAGIGRCP	111			
83	LSTTRFQLNCTCETST	TPRCPYSSRTEIN YICVKENQYVHFAGIGRCP	133			
Db						
RESULT 2						
LECS RANJA						
ID	LECS RANJA	STANDARD;	PET;	111	AA.	
AC	P18839;					
DT	01-NOV-1990	(Rel. 16,	Created)			
DT	01-FEB-1994	(Rel. 28,	Last sequence update)			
DT	10-OCT-2003	(Rel. 42,	Last annotation update)			

Sialic acid-binding lectin (EC 3.1.27.-).
Rana japonica (Japanese reddish frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI TaxID=8402;
[1]_SEQUENCE, AND DISULFIDE BONDS.
RN
RP
RT
RC
RX
RX
RX
RX
RA
RA
RA
RT
RT
RT
RT
CC
CC
CC
CC
CC

CC	-1- SUBUNIT: Monomer.	
CC	-1- SUBCELLULAR LOCATION: Secreted.	
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.	
DR	PIR; JX0120; JX0120.	
DR	HSSP; P11916; IBC4.	
DR	InterPro; IPR001427; RNaseA.	
DR	Pfam; PF00074; rnaseA; 1.	
DR	ProDom; PD000535; RNaseA; 1.	
DR	SMART; SM00092; RNase PC; 1.	
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.	
KW	Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;	
KW	Pyrolysine carboxylic acid. PYROLIDONE CARBOXYLIC ACID.	
FT	MOD RES 1 1	
FT	ACT SITE 10 10	BY SIMILARITY.
FT	ACT_SITE 35 35	BY SIMILARITY.
FT	ACT_SITE 104 104	BY SIMILARITY.
FT	DISULFID 19 72	
FT	DISULFID 34 82	
FT	DISULFID 52 97	
FT	DISULFID 94 111	
FT	SEQUENCE 111 AA; 123226 MW; FDEBDDF3834ED679 CRC64;	
SO		

[illegible]

RESULT 3	
ID	RNPL RANCA STANDARD; PRT; 111 AA.
AC	P14636;
DT	01-APR-1990 (Rel. 14, Created)
DDT	01-FEB-1994 (Rel. 28, Last sequence update)
DDT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Ribonuclease, liver (EC 3.1.27.5).
DE	Rana catesbeiana (Bull frog).
OC	Rana catesbeiana [Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
OC	NCB1_taxid=8400;
OX	[1]
RN	SEQUENCE.
RP	TISSUE=Liver;
RC	MEDLINE=90130374; PubMed=2613682;
RX	Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA	Okazaki T., Ohgi K., Irie M.;
RA	"primary structure of a ribonuclease from bullfrog (<i>Rana catesbeiana</i>)
RT	liver."

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:30:40 ; Search time 5.60711 Seconds
(without alignments)
1030.796 Million cell updates/sec

Title: US-09-961-400-17

Perfect score: 607

Sequence: 1 MQNWATQKHIIPTICN.....ICVKENQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	591.5	97.4	133	1	RNPO_RANCA
2	455	75.0	111	1	LECS_RANJA
3	374	61.6	111	1	RNPL_RANCA
4	277.5	45.7	104	1	RN30_RANPI
5	154.5	25.5	145	1	ANGR_MOUSE
6	149.5	24.6	145	1	ANGR_MOUSE
7	135.5	22.3	124	1	RNP_BALAC
8	135.5	22.3	124	1	ANGI_MOUSE
9	133.5	22.0	167	1	RNBR_BOVIN
10	132.5	21.8	124	1	RNP_FIG
11	131.5	21.7	119	1	RNP_IGUIG
12	128.5	21.2	151	1	RNBR_CAPCA
13	127.5	21.0	123	1	ANG2_BOVIN
14	127.5	21.0	141	1	RNBR_GIRCA
15	127.5	21.0	151	1	RNBR_AXIPR
16	125	20.6	146	1	ANGI_SALSC
17	124	20.4	146	1	ANGI_MIOIA
18	123.5	20.3	143	1	RNBR_SHEEP
19	122.5	20.2	124	1	RNP_ANTAM
20	122.5	20.2	146	1	ANGI_CERAE
21	122	20.1	122	1	RNP_MACRU
22	120.5	19.9	128	1	RNP_WYOCO
23	120.5	19.9	149	1	RNP_MOUSE
24	120	19.8	146	1	ANGI_AOTTR
25	120	19.7	147	1	ANGI_PONPY
26	119.5	19.7	123	1	ANGI_PIG
27	118.5	19.5	128	1	RNFB_CAVPO
28	118	19.4	146	1	ANGI_SAGEO
29	117.5	19.4	128	1	RNP_HORSE
30	116.5	19.2	124	1	RNP_CAMDR
31	116.5	19.2	128	1	RNP_PROGU
32	115.5	19.0	119	1	RNS4_BOVIN
33	115.5	19.0	146	1	ANGI_MACWU
					Q8wn63 macaca mulla

34 114 18.8 148 1 ANGI_BOVIN
35 113.5 18.7 124 1 RNP_RANTA
36 113.5 18.7 146 1 ANGI_PAPHA
37 113 18.6 147 1 ANGI_HUMAN
38 113 18.6 147 1 ANGI_PANTR
39 112.5 18.5 124 1 RNP_CAPCA
40 112.5 18.5 124 1 RNP_GIRCA
41 112.5 18.5 148 1 RNS4_MOUSE
42 112 18.5 125 1 ANGI_RABIT
43 111.5 18.4 130 1 RNP_CRILO
44 111.5 18.4 147 1 RNS4_RAT
45 111.5 18.4 149 1 RNP_ACOCA

ALIGNMENTS

RESULT 1
RNPO_RANCA STANDARD; PRT; 133 AA.
AC P11916; Q9PWR7;
DT 01-OCT-1989 (Rel. 12, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes precursor (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SHL-C).
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165825; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
[2]
RP SEQUENCE OF 23-133.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs";
RL Biochemistry 26:2189-2194(1987).
RN [3]
RP CHARACTERIZATION, AND SEQUENCE OF 81-101.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [4]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [5]
RP STRUCTURE BY NMR OF 23-133.
RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
RN [6]
RP FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine

```
QY 34 CKVNTFISSATVKAICTG----VINNVLSSTRFQNTCTRTSITPR-PCPYSSRTE 88
DB 39 CKVNTFIHGTRNDIKAKCNKNGEPYNNPRRSKSPFQITTCCKHKGSGNRPCCGYRATAG 98
QY 89 TNYICVKCENQYVHF 104
DB 99 FRTIIVACENGLPVHF 114

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N;Alternate names: RNase IB
C;Species: Cavia porcellus (guinea pig)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C;Accession: A00826
R;van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A;Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure a
A;Reference number: A91247; MUID: 77185023; PMID: 862624
A;Accession: A00826
A;Molecule type: protein
A;Residues: 1-128 <VAN>
A;Note: 64-Pro was also found
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match 19.5%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

QY 7 FQOKHI-----INTPIICNTIMDNINXIVGGQCKRVNTFISSATVKAICTGVINNVN 60
DB 8 FQRQHMDEGSPSNSSNYCNVMMIRR-NNTQGRCKPNTFVHESLADVQAVC---FQKNV 63
QY 61 L-----STTRFQNTCTRTSITPR-CPYSSRTETNYICVKCENQ--YVVF 104
DB 64 LCKNGQTCYQYSRMRITDCRVTSKFPNGSYRMSQAKSIIVACEGDPYVVF 120

Search completed: May 7, 2004, 21:54:55
Job time : 10.072 secs
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Sat May 8 17:57:16 2004

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Db 6 AKFERQHIDSNPSSVSSSYNNYCNQMKSR-NLTQGRCKPVNTFVHESLADVQAVCS---QK 61
QY 59 NVL-----STTRFQLNTCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104
Db 62 NVACKNGQNCYQSYSTMSITDCRETGSSKYPNCAYKTTQAKKHIIIVACEGPNYPVPHY 120

RESULT 11
NRKGR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N;Alternate names: RNase 1; RNase A
C;Species: Macropus rufus, Megaleia rufa (red kangaroo)
C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C;Accession: A00833
R;Gaaststra, W.; Wellington, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A;Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A;Reference number: A00833; MUID:78190621; PMID:658039
A;Accession: A00833
A;Molecule type: protein
A;Residues: 1-122 <GAA>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;11,40,117/Active site: His, Lys, His #status predicted
F;25-83,39-94,57-109,64-71/Disulfide bonds: #status predicted
F;61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 18; Gaps 6;

QY 7 FQQRHI-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKATC-----52
Db 7 FQRQMDTEHSTASSYCNLMKAR-DMTSGRCKPLNTFHEPKSVVDVACHGENTCK 65

QY 53 TGVNNMVLSTTRFQLNTCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104
Db 66 NGRINC-YKSNRLSITNCRQTGASKYPCQYETSLNKLIIIVACEGQYVPVHF 118

RESULT 12
NRKU
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Myocastor coypus (nutria, coypu)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C;Accession: A00822
R;van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A;Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A;Reference number: A90612; MUID:77065676; PMID:999896
A;Accession: A00822
A;Molecule type: protein
A;Residues: 1-128 <VAN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F;34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

QY 7 FQQRHI-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKATCTGVNNMV 60
Db 8 FQRQMDSRGSPSTNNYCNQMKSR-NMTQGRCKPVNTFVHESLADVQAVC---FQRNV 63

QY 61 L-----STTRFQLNTCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104
Db 64 LCKNGQNCYQSNMHIIDCRVTSNDSYPCYSQEEKSIIVACEGPNYPVPHY 120
```

RESULT 13

NRMS

```
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N;Alternate names: RNase 1; RNase A
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C;Accession: A34090; S22598; A00830
R;Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A;Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A;Reference number: A34090; MUID:90136034; PMID:2299980
A;Accession: A34090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-149 <SCH>
A;Cross-references: GB:M27814; NID:G200762; PIDN:AAA40060.1; PID:G200763
R;Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A;Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A;Reference number: S22598; MUID:92107684; PMID:1840677
A;Accession: S22598
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-149 <SAM>
A;Cross-references: EMBL:X60103; NID:G53981; PIDN:CAA42697.1; PID:G53982
R;Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 98, 399-408, 1979
A;Title: The amino acid sequence of mouse pancreatic ribonuclease.
A;Reference number: A00830; MUID:80024269; PMID:556267
A;Accession: A00830
A;Molecule type: protein
A;Residues: 26-149 <LEN>
C;Superfamily: pancreatic ribonuclease
C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F;37,66,144/Active site: His, Lys, His #status predicted
F;51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted
F;62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

QY 7 FQQRHI-----INTPIICNTIMDNNIYVGGCKRVNTFISSATTVKATCTGVNNMV 60
Db 33 FQRQMDPDGSSINSPTYCNQMKRR-DMTGSCPKPVNTFVHEPLADVQAVCS---QENV 88

QY 61 L-----STTRFQLNTCTRTSITPRP-CPYSSRTENYICVKCE-NOY-PVHF 104
Db 89 TCKRKSNCYKSSSALHITDCHLKGSKYPNCYKDYKTYQKHIIIVACEGPNYPVPHF 145

RESULT 14
A43825
angiogenin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: S29834; A43825
R;Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A;Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernmer
A;Reference number: S29833; MUID:93192291; PMID:8448182
A;Accession: S29834
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-123 <BON>
A;Note: this sequence was submitted to the Protein Sequence Database, December 1992
C;Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;
```

S20066

pancreatic-type ribonuclease (EC 3.1.27.5) BRB precursor, brain - bovine
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
 C:Accession: S20066; JX0056

R:Sasso, M.P.; Carsana, A.; Confalone, E.; Cossi, C.; Sorrentino, S.; Viola, M.; Palmieri
 Nucleic Acids Res. 19, 6469-6474, 1991
 A:Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
 A:Reference number: S20066; MUID:92093604; PMID:1754384

A:Accession: S20066
 A:Molecule type: DNA
 A:Residues: 1-167 <SAS>

A:Cross-references: EMBL:X59767; NID:gl50; PIDN:CAA42439.1; PID:gl51
 R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri

J. Biochem. 104, 939-945, 1988
 A:Title: Primary structure of a ribonuclease from bovine brain.

A:Reference number: JX0056; MUID:89214015; PMID:3243767

A:Accession: JX0056

A:Molecule type: protein

A:Residues: 27-154, 8', 156-166 <WAT>

A:Experimental source: brain

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase

F:38,67,145/Active site: His, Lys, His #status predicted

F:52-110,66-121,84-136,91-98/Disulfide bonds: #status predicted

F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental

F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 22.0%; Score 133.5; DB 2; Length 167;

Best Local Similarity 31.4%; Pred. No. 3.6e-06;

Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 5 ATFOQKH-----INTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVNM 58

Db 32 AKFRQHMDSGSSSSPNVCNQMKER-RMTHGRCKPVTFFVESLDDVRAVCS---QK 87

QY 59 NVL-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHFA 105

Db 88 NITCKNGHPNCYQSKSTMSITDRETGSSKYPNCAYKTSQKQYITVACSGNPVPVHFD 147

QY 106 G 106

Db 148 G 148

RESULT 8

NRPRH

pancreatic ribonuclease (EC 3.1.27.5) - pig

N:Alternate names: RNase A

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994

C:Accession: A92071; A91391; A00816

R:Jackson, R.L.; Hirs, C.H.W.

J. Biol. Chem. 245, 637-653, 1970

A:Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se

A:Reference number: A92071; MUID:70104197; PMID:5460946

A:Accession: A92071

A:Molecule type: protein

A:Residues: 1,'Q',3-124 <JAC>

R:Wierenga, R.K.; Huizinga, J.D.; Gaastera, W.; Welling, G.W.; Beintema, J.J.

FEBS Lett. 31, 181-185, 1973

A:Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation

A:Reference number: A91391

A:Accession: A91391

A:Molecule type: protein

A:Residues: 1-124 <WIB>

R:Phelan, J.J.; Hirs, C.H.W.

J. Biol. Chem. 245, 654-661, 1970

A:Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo

A:Reference number: A92072; MUID:70104198; PMID:4904878

A:Contents: annotation; disulfide bonds

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
 F:12,41,119/Active site: His, Lys, His #status predicted
 F:21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:26-84,40-95,58-110,65-72/Disulfide bonds: #status experimental

Query Match 21.8%; Score 132.5; DB 1; Length 124;

Best Local Similarity 31.6%; Pred. No. 3.3e-06;

Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FOQKH-----INTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGV-INNN 59

Db 8 FQEQHMDPDSSSSNSVNCNLMWSRR-NMTGRCRCPVTFFVESLADVQVCSQINVNCK 66

QY 60 VLSITRFPNT-----CTRTSITPRP-CPYSSRTETNYICVKCE-NQ--VPVHF 104

Db 67 NGQTNCYQSNSTMHITDCRQTGSSKYPNCAYKASQEQKHIIIVACSGNPVPVHF 120

RESULT 9

S41111

pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998

C:Accession: S41111

R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.

Eur. J. Biochem. 219, 641-646, 1994

A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.

A:Reference number: S41111; MUID:9413745; PMID:8307028

A:Accession: S41111

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-119 <ZHA>

C:Superfamily: pancreatic ribonuclease

Query Match 21.7%; Score 131.5; DB 2; Length 119;

Best Local Similarity 30.4%; Pred. No. 4e-06;

Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 2 QNWATFOQKH-----INTPIICNTIMDNIIYVGQCKRVNTFISSATTVKAIC-- 52

Db 1 QDWSSFNKHIDYDTPETSSAPNAYCDLMQRR-NLAPTKCKTRNTFVHASPFIQQVCS 59

QY 53 --TGVINMVLTSTRFQNTCTRTSIT-PRCPYSSRTETNYICVKCE-NQVPVHF 104

Db 60 GPHYEDNLYDSNESFDLTCKNVGTAFTSSCKYNGTPGTGRIACENQPVHF 114

RESULT 10

NRPRH

pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Antilocapra americana (pronghorn)

C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000

C:Accession: A00813

R:Beintema, J.J.; Gaastera, W.; Munniksma, J.

J. Mol. Evol. 13, 305-316, 1979

A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BEI>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12,41,119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.2%; Score 122.5; DB 1; Length 124;

Best Local Similarity 30.3%; Pred. No. 3.3e-05;

Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY 5 ATFOQKHINTPI-----ICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVNM 58

QY 2 QNWATFOQKHINTP-IICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGV-INNN 59
Db 1 QNWAKFQKHINTPNTGNCINNTIMDSIIYVGGCKRVNTFISSATTVKAICTGASTRN 60

QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 61 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNRLPVHFGIGRC 111

RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg
J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.6%; Score 374; DB 2; Length 111;
Best Local Similarity 65.8%; Pred. No. 2.8e-30;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

QY 2 QNWATFOQKHINTP-II-CNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-INNN 59
Db 1 QNWAKFQKHINTPNTGNCINNTIMDSIIYVGGCKRVNTFISSATTVKAICTGASTRN 60

QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 61 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNRLPVHFGIGRC 111

RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 45.2%; Score 274.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.1e-20;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

QY 2 QNWATFOQKHINTP-II-CNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-INNN 59
Db 1 EDWLTFQKHINTPNTGNCINNTIMDSIIYVGGCKRVNTFISSATTVKAICTGASTRN 60

QY 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHFAGIGRC 110
Db 57 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNRLPVHFGIGRC 104

RESULT 5
NRWKK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale

N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmons, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
F:26-84,40-95,110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.3%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

QY 7 FQOKHII-----NTPICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-INNN 60
Db 8 FQOKHII-----NTPICNTIMDNIIYVGGCKRVNTFISSATTVKAICTGVI-INNN 60

QY 61 L-----STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCNQYVPHF 104
Db 64 LCKNGRTNCVSNSTWHITDCRQTGSSKYPNCAYKTSQKEKHIIIVACEGNYVPHF 120

RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
A:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37,64,137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.3%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

QY 34 CKRVNTFISSATTVKAIC---TGVIINNNV-LSTTRFQNTCTRTSITPR-PCPYSSRT 88
Db 63 CKRVNTFIHGKSNKAIKAGANGSPYRNLMSKSPFQVTTCKHTGGSPRPCCQYRASAG 122

QY 89 TNYICVKCNQYVPHF 104
Db 123 FRHVVIACENGLFVHF 138

RESULT 7

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 7, 2004, 21:38:36 ; Search time 10.072 Seconds
(without alignments)
1060.090 Million cell updates/sec

Title: US-09-961-400-17
Perfect score: 607
Sequence: 1 MQNWATFOQKHINTPIICN.....ICVKCENQYPVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:**

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.0	111	2	A27121
2	455	75.0	111	1	JX0120
3	374	61.6	111	2	JX0085
4	274.5	45.2	104	2	A39035
5	135.5	22.3	124	1	NRWHK
6	135.5	22.3	145	1	A35932
7	133.5	22.0	167	2	S20066
8	132.5	21.8	124	1	NRPG
9	131.5	21.7	119	2	S41111
10	122.5	20.2	124	1	NRPRH
11	122	20.1	122	1	NRKGR
12	120.5	19.9	128	1	NRGU
13	120.5	19.9	149	1	NRMS
14	119.5	19.7	123	1	A43825
15	118.5	19.5	128	1	NRGPB
16	117.5	19.4	128	1	NRHO
17	116.5	19.2	124	1	NRGM
18	116.5	19.2	124	1	NRMM
19	116.5	19.2	124	1	NRMB
20	116.5	19.2	124	1	NRKS
21	114.5	18.9	124	2	S08549
22	114	18.8	125	1	A32474
23	113.5	18.7	124	1	NRDEN
24	113	18.6	147	1	NRHUG
25	112.5	18.5	124	1	NRGF
26	112.5	18.5	124	1	NRDEO
27	112	18.5	125	1	B43825
28	111.5	18.4	130	2	S22808
29	110.5	18.2	124	1	NRBOB

30 110.5 18.2 124 1 NRWB pancreatic ribonuc
31 110.5 18.2 124 1 NREKN pancreatic ribonuc
32 110.5 18.2 124 2 S07141 pancreatic ribonuc
33 110.5 18.2 150 1 NRBO pancreatic ribonuc
34 110.5 18.2 158 2 I61900 eosinophil-derived
35 109.5 18.0 124 1 NRSH pancreatic ribonuc
36 108.5 17.9 119 2 JX0115 pancreatic ribonuc
37 108.5 17.9 124 1 NRCB pancreatic ribonuc
38 108.5 17.9 152 1 NRRT pancreatic ribonuc
39 106.5 17.5 124 1 NRHP pancreatic ribonuc
40 106.5 17.5 125 4 A47498 seminal ribonuclea
41 106.5 17.5 150 1 NRBO5 pancreatic ribonuc
42 104.5 17.2 124 1 NRDEF pancreatic ribonuc
43 104.5 17.2 125 2 S04503 pancreatic ribonuc
44 104 17.1 124 2 S08546 pancreatic ribonuc
45 103.5 17.1 124 2 S08546 pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C:Accession: A27121
R;Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi
A;Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A;Reference number: A27121; MUID:87299649; PMID:3304421
A;Accession: A27121
A;Molecule type: protein
A;Residues: 1-111 <TIT>
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin

Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 1.3e-51;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 2 QNWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMV 60
Db 1 ENWATFOQKHINTPII-CNTIMDNNIYVGGCKRVNTFISSATVKAICTGVINMV 60
QY 61 LSTTRFQNLTCRTSITPRCPYSKRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 LSTTRFQNLTCRTSITPRCPYSKRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2

JX0120
ribonuclease-related sialic acid-binding lectin - Japanese frog
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R;Kamiya, I.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi,
J. Biochem. 108, 139-143, 1990
A;Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A;Reference number: JX0120; MUID:91035319; PMID:2229005
A;Accession: JX0120
A;Molecule type: protein
A;Residues: 1-111 <KAM>
A;Experimental source: egg
C;Superfamily: pancreatic ribonuclease
C;Keywords: lectin; pyrrolutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.0%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2.5e-38;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

Sat May 8 17:57:16 2004

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
; OTHER INFORMATION: Met(-1) RapLRI)
US-09-948-391A-6
Query Match      47.2%; Score 286.5; DB 10; Length 105;
Best Local Similarity 50.0%; Pred. No. 7.5e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 1 MOWWTFQOKHIINT-PIICNTIMDNINIVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MQDWLTFQKHLINTRDVDCNNIMSTNLP----HCKDKNTFIYSRPEPVKAICKGLIASK 56
QY 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFGIGRC 110
Db 57 NVLTTSEFYLSDC--NVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGHG 105

```

Search completed: May 7, 2004, 21:51:58
 Job time : 36.6155 secs

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match 98.4%; Score 597; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 3.1e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVLS 62
DB 2 NWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVLS 61

QY 63 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 13
US-09-961-400-19
Sequence 19, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match 98.2%; Score 596; DB 10; Length 110;
Best Local Similarity 98.2%; Pred. No. 4e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 61
DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60

QY 52 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 51 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 14
US-09-948-391A-19
Sequence 19, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 1999-03-26
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana
OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
OTHER INFORMATION: Met57Leu substitutions (recombinant RacORI
OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match 97.2%; Score 590; DB 10; Length 110;
Best Local Similarity 97.3%; Pred. No. 2e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QNWATFOQKHINTPIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMNVL 61
DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNL 60

QY 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-6
Sequence 6, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 105